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Million cell updates/sec
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Adn22998 Bacterial
Aab47250 Human pp7
Adt66673 Human pro
Adj95096 Novel NOV
Adj95098 Novel NOV
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Abb63840 Drosophil
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AAE16244 AAE16236 AAE09733 AAE09731 AAE09732 ADS44165

Aae16236 Aae16244

genes from Dr interactions.

Disclosure; SEQ ID NO 41259; 21pp + Sequence Listing; English.

New isolated nucleic acid genes from Drosophila and

detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell

WPI; 2001-656860/75. N-PSDB; ABL15592.

ADN21438 ABG09988 ABR53882

Protein Novel hum

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL016176-ABL301511), expressed DNA sequences (ABL016176-ABL301511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

invention

and 18

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Adx79431 Plant ful	Adx67181 Plant ful	Aag39549 Arabidops	Adn23944 Bacterial	Adn19921 Bacterial	Ady06935 Plant ful	Ady10803 Plant ful	Plant			Ady22333 Plant ful	Ady08660 Plant ful	_	Ady09284 Plant ful		Aag30062 Arabidops	Adx87721 Plant ful	Abp98033 Protein p	Ads23974 Bacterial	Abb59732 Drosophil	Ads43550 Bacterial

ALIGNMENTS

## RESULT 1 ABB71489 Venter JC, 23-MAR-2000; 2000US-0191637P 11-JUL-2000; 2000US-00614150 23-MAR-2001; 2001WO-US009231. Drosophila melanogaster. pharmaceutical. Drosophila; developmental biology; cell signalling; insecticide; Drosophila melanogaster polypeptide SEQ ID NO 41259. 26-MAR-2002 ABB71489; ABB71489 standard; protein; 637 AA. 27-SEP-2001. WO200171042-A2 (PEKE ) PE CORP NY. Adams M, (first entry) 닭 PWD, Myers 竖

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RESULT 2
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Best Local Simi
Matches 637;
                                                   Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
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---LPIRKNHIDLLIDVFRKKRGNRLHPKYVALIILRBAAKSLKQLPNISPVSTAVSQQVT
-|--LPIRKNHIDLLIDVFRKKRGNRLHPKYVALIILRBAAKSLKQLPNISPVSTAVSQQVT

AMAEENGKGGVENGRNSPLMSALSHYAKPSLMDSEGETVKKMLEDTSPTNVDIDRNYKGP HMPQAAGRKNQYQG--SAHVSVLDD--KDDLVEEFGDIVNAKIE------STIKSAILIQKWYRRCBARLBARRATWQIFTALBYAGBQDQLKVRVWITLYDFFADVIR

TLSLPLDKPQVAKMIEAF--KVNKVLHPKYVLMILHEARKIFKAMPSVSRISTSISNQVT

| CGDLHGKFDDLCIILYKNGYPSVDNPYIFNGDFVDRGGQSIEVLCVLFALVIVDPMSIY

327 214 267 154 209 97

VCGDLHGKLDDLLVVLHKNGLPSSSNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVF

LNRGNHEDHIMNLRYGFIKELSTKYKDLSTPITRLLEDVFSWLFIATIIDRDIFVVHGGI LNRGNHEDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGF 맑 Ś

90 4,

NAIRAAIFIQKWYRRHQARREMQRRCNWQIFQNLEYASBQDQAB-----LYKFFNDLIK 57

Query Match Best Local Similarity Matches 266; Conserv

Conservative 117;

37.9%; Score 1305; DB 8; 41.6%; Pred. No. 9.6e-114;

Length Indels

Mismatches

56;

Gaps

149

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CC promoter functional in a plant cell, where the promoter is positioned to comprise source. The invention also relates to a transformed plant cell comprising the recombinant DNA construct and a method of producing a crop plant cell transformed plant cell transformed plant cell transformed plant is a crop plant cell as maize or soybean. The method of producing a transformed plant cell thaving an improved property. The plant is a crop plant cell thaving an improved property comprises transformed plant is a crop plant cell thaving an improved property comprises transformed plant, where the cell cylnucleotide or polypeptide is useful for improving plant properties. CC The recombinant DNA construct is useful for producing plant with the cell comproved plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of concent, improved yield by modification of carbohydrate, nitrogen or content, improved yield by modification of carbohydrate, nitrogen or content, improved plant growth and development under at least one stress condition, improved lignin production of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production of photosynthesis or by growth in invention. Note: The sequence data for this patent did not complete the printed specification but was obtained in electronic company of the printed specification but was obtained in electronic company of the printed specification but was obtained in electronic company of the printed specification but was obtained in electronic company of the printed specification but was obtained in electronic company of the printed specification but was obtained in electronic company of the printed specification because of the company o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant DNA construct comprising a promoter positioned to provi
for expression of a polynucleotide encoding a polypeptide from a
microbial source, useful for producing plants with improved properties.
Sequence
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(HINK/)
(SLAT/)
(CHEN/)
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26-OCT-1999;
07-SEP-2000;
This sequence shows a protein containing calmodulin/calcium binding motifs which was identified using the method of the invention. The method comprises a computer system for extracting information from biological sequence databases, which receives a motif that defines a desired polypeptide sequence. The computer searches the database based on a que formulated from the motif to obtain a set of polypeptide sequences which are then filtered and a report of the filtered set of polypeptide sequence information is then displayed. The computer system is useful identifying recombinant C.elegans p95.6/YN52 and other mitochondrial
                                                                                                                                                                                                                                                                                                                               New Caenorhabditis elegans mitochondrial calcium-binding protein, p95.6/YN52, identified by protein motif database searching, usefur regulating intracellular calcium ions and in drug screening assay
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g; sequence extraction; PP7; calcium binding m
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HIDDSQVNKLANIMDLNKDGSIDENEFLKAFYV--VHRYB
                            AYSKAEMLEKCRMMDLNGDGKVDLNEFLEAFRLSDLHRKE
                                                                                     DTD-VILEAEADGMSVMDALYANKASLVAIFNIIDADNSGEITLDEFETAIDLLVAHMPG
                                                                                                                                              LEDEFRKYDPKDSGYISISHWCKVMENVTKLGLPWRLLRDKLAPGTDSQKVNYNRTLDLL
                                                                                                                                                                           SNRGAYIKLCSGTTPRFFQY----QVTKATCFQPLRQRVDTMENSAIKILRERVISRKSD
                                                                                                                                                                                                    SNKGAYIRLNNQLMPHFVQYISAASQTKRLSF---KQRMGIVBSSALKELAVRMRDHRDB
                                                                                                                                                                                                                                   PNTCRGGGCYFGPDVTSKILNKYQLKMLIRSHECKPEGYEICHDGKVVTIFSASNYYEEG
                                                                                                                                                                                                                                                              PNTLRGAGVWFGPDVTDNFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNYYAIG
                                                                                                                                                                                                                                                                                                                                                  KYKLHGKRILQILEEFYAWLFIGTIVDNEILVIHGGISETTDLNLLHRVERNKMKSVLIF
                                                                                                                                                                                                                                                                                                                                                                       KYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGFSDSTSLDLIKSIDRGKYVSILRP
                                                                                                                                                                                                                                                                                                                                                                                                            ERNPYVFNGDFVDRGKNSIBILMILCVSFLVYPNDLHLNRGNHEDFMMNLRYGFTKBILH
                                                                                                                                                                                                                                                                                                                                                                                                                              SSNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNARYGFIREVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NRLHPKYVALILREAAKSLKOLPNISPVSTAVSQQVTVCGDLHGKLDDLLVVLHKNGLPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HKEELELRNQSLESEQDMRDRWDYVDSIDVPDSYNGPRLQFPLTCTDIDLLLEAFKEQQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGRKNQYQGSAHVSVLDDKD--DLVB--BFGDIVNA-KIBLPIRKNHIDLLIDVFRKKRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DTSLRAALIIQNWYRGYKARLKARQHYALTIFQSIBYADEQGQMQLSTFFSFMLBNYTHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENAIRAAIFIQKWYRRHQARREMQRRCNWQIFQNLEYASEQDQAELYKFFNDLIKHMPQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      653
                                                                                                                  LTRAFQLQDHRKSGKLSVSQWAFCMENILGLNLPWRSLSSNLVNIDQNGNVEYMSSFQNI
                                                                                                                                                                                                                                                                                          PTETNRDHDTDSKHNKVGVTFNAHGRIKTNGSPTEHLTEHEWEQIIDILWSDPRGKNGCF
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                                                         -TLVETLYRYRSDLEIIFNAIDTDHSGLISVEEFRAMWKLFSSHYNV
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1271.5; DB 4
No. 1.2e-110;
                                                                                                                                                                                                                                                                                                                    -TDGEP---LDKTEWQQIFDIMWSDPQATMGCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204;
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                                                          60%
                                                                                                                   547
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ADT66673 standard; protein; 653 ₿

ADT66673;

16-DEC-2004 (first entry

protein phosphatase, ΒF hands-1 protein.

ADT6667 ADT6673 ID ADT6 XX ADT6 XX ADT6 XX ADT6 XX Hume XX Hume XX Hume XX Hume XX Hume XX Hume XX Bair KW Pair KW neuru KW Neuru KW Synth pain regulation; screening; LuzP; PEP-19; phosphatidylinositol synthase; valosin; interleukin 6 receptor subunit beta; aspartate aminotransferase; neuronal immediate early gene; heat shock protein 27; HSC70; calmodulin; syntaxin binding protein 1; spliceosomal protein SAP 155; neurodap 1; bamacan; leukotriene A4 hydrolase; chondromodulin 1; Ms84/phosphatidylinositol-4-phosphate 5 kinase; 265 proteasome UE p112; UE Z; UE p44.5; ingensin; 3-hydroxy-3-methylgluaryl-Co A synthase; phosphoglycerate kinase; RNA polymerase II TF SIII p18 UE;

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This invention describes novel polynucleotides and polypeptides involved compounds for therapy and diagnosis. Identifying pain-regulating compounds for the protein and/or compress incubating a test compound with a cell, and/or correct, then measuring either binding of test compound to the protein or correct, then measuring either binding of test compound to the protein is one correct, then measuring either binding of test compound to the protein or correct, then measuring either binding of test compound to the protein or correct, then measured either binding of test compound to the protein or correct, then measured either binding of test compound to the protein is one correct, the protein or correct, the protein is one correct, the protein or containing protein interleukin of receptor submit betta, aspartate containing protein, interleukin of receptor submit betta, aspartate protein containing protein interleukin of receptor submit betta, aspartate containing protein spatial protein save protein spatial protein save protein spatial protein spatial correct phosphatase payabatis, 3-hydroxy--methylgluaryl-co A synthase, 12 or UE payabatase, 12 protein, 3-hydroxy--methylgluaryl-co A synthase, 12 or UE payabatase, 12 protein, 3-hydroxy--methylgluaryl-co A synthase, 12 correct phosphatase, 12 protein, 3-hydroxy--methylgluaryl-co A synthase, 12 correct phosphatase, 12 protein, 3-hydroxy--methylgluaryl-co A synthase, 12 correct phosphatase, 12 protein, 13 protein save used factor 6-binding protein, 13 protein spatial used protein synthase, 12 protein, 13 protein spatial used 10 protein, 13 protein spatial used 10 protein, 13 protein spatial protein spatial protein spatial protein spatial protein spatial protein spatial display PCR method (13 protein spatial display PCR method (13 protein spatial protein spatial spatial protein 
                                                                                                                                                          Query Match
Best Local Simi
Matches 258;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transcription co-activator CRSP150; JERKY; SOUL protein; rRNA intron-encoded homing endonuclease; epithelial cell growth inhibitor; glutathione transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides and polypeptides involved in pain regulation, useful in screening for pain-regulating compounds for therapy and diagnosis.
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                                                  ENAIRAAIFIQKMYRRHQARREMQRRCNWQIFQNLEYASEQDQAELYKFFNDLIKHMPQA
DTSLRAALIIONWYRGYKARLKAROHYALTIFOSIEYADEOGOMOLSTFFSFMLENYTHI
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                                                                                                                                                              Conservative 129;
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40.3%;
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                                                                                                                                                          Score 1271.5;
Pred. No. 1.2e.
29; Mismatches
                                                                                                                                                                                               5; DB 8;
                                                                                                                                                          Indels
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HIDDSQVNKLANIMDLNKDGSIDFNBFLKAFYV--VHRYB
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                                                                                                                                          DTD-VILEABADGMSVMDALYANKASLVAIFNIIDADNSGBITLDBFBTAIDLLVAHMPG
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                                               AYSKABMLEKCRMMDLINGDGKVDLINEFLEAFRLSDLHRKE
                                                                                              RIEKPVQEAHS---TLVETLYRYRSDLEIIFNAIDTDHSGLISVEEFRAMWKLFSSHYNV
                                                                                                                                                                                                                                                                                                                                       SNKGAYIRLNNQLMPHFVQYISAASQTKRLSF---KQRMGIVESSALKELAVRMRDHRDE
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                                                                                                                                                                                              LTRAPQLQDHRKSGKLSVSQWAPCMENILGLNLPWRSLSSNLVNIDQNGNVEYMSSFQNI
                                                                                                                                                                                                                                        LEDEFRKYDPKDSGYISISHWCKVMENVTKLGLPWRLLRDKLAPGTDSQKVNYNRTLDLL
                                                                                                                                                                                                                                                                                       SNRGAYIKLCSGTTPRFFQY----QVTKATCFQPLRQRVDTMENSAIKILRERVISRKSD
                                                                                                                                                                                                                                                                                                                                                                                      PNTCRGGGCYFGPDVTSKILNKYQLKMLIRSHECKPEGYEICHDGKVVTIFSASNYYEEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -TDGEP---LDKTEWQQIFDIMWSDPQATMGCV
                                                 604
  642
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ADJ95096 standard; protein; 613
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Novel NOVX protein sequence #162. 06-MAY-2004 (first entry)

asthma; dyslipidemia; neurogenesis; cell differentiation; cell proliferation; hematopolesis; wound healing; angiogenesis; chromosome mapping; tissue typing; pharmacogenomic. hypertension; atherosclerosis; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder; osteoarthritis; hematopoietic disorder; inflammatory skin disorder; anorectic; virucide; antibacterial; fungicide; protozoacide; noot neuroprotective; antiparkinsonian; anticonvulsant; osteopathic; antiarthritic; antiinflammatory; dermatological; antiasthmatica; antilipemic; gene therapy; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer; cardiovascular disease; antidiabetic; anorectic; cardiant; hypotensive; antiarteriosclerotic; nootropic;

15-MAY-2003.

05-NOV-2002; 2002WO-US035464

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05-NOV-2001
06-NOV-2001
06-NOV-2001
15-NOV-2001
16-NOV-2001
20-NOV-2001
21-NOV-2001
22-NOV-2001
28-NOV-2001
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29-NOV-2001
30-NOV-2001
30-NOV-2001
30-NOV-2001
10-DEC-2001
10-DEC-2001
11-DEC-2001
11-DEC
                                                                                                                                                                                                                                                                                                                      Agee ML,
Chaudhuri
                                                                 preventing, diagnosing or treating NOVX-a osteoarthritis, obesity, atherosclerosis,
                                                                         New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
                                                                                                                                                                                                                                                                                                   Gangolli
                  Claim 1;
                                                                                                                                                            2003-441551/41.
DB; ADJ95095.
                                                                                                                                                                                                                   II, Alsobrook JP, Berghs C, Boldog FL, Burgess CE, Chan uri A, Dipipo VA, Edinger SR, Elsen A, Ellerman K; Li EA, Gorman L, Gerlach VL, Ji W, Kekuda R, Khramtsov Malyankar UM, Macdougall JR, Mezes PS, Miller CE, Mill, Ort T, Padigaru M, Patturajan M, Rastelli L, Rieger berg ME, Shenoy SG, Spaderna SK, Spytek KA, Taupier RJ; CAM, Zerhusen BD, Zhong M;
                                                                                                                                                                                                                                                                                                                                                                                   CURAGEN CORP.
                  SEQ
                                                           infections
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2001US-033972P.
2001US-0335610P.
2001US-0335610P.
2001US-0331641P.
2001US-0331641P.
2001US-033162P.
2001US-033421P.
2001US-033421P.
2001US-033420P.
2001US-033420P.
2001US-033420P.
2001US-0334526P.
2001US-0336664P.
2001US-0336664P.
2001US-0338390P.
2001US-0339906P.
2001US-0339906P.
2002US-0354393P.
2002US-0354393P.
2002US-0354393P.
2002US-0364182P.
2002US-0401552P.
2002US-0401552P.
2002US-0405496P.
2002US-0405496P.
2002US-0406623P.
2002US-0406631P.
2002US-0406631P.
2002US-0405631P.
2002US-0405631P.
2002US-0405631P.
2002US-0405631P.
2002US-0405631P.
                  ID NO 324;
              4 dd008
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A, Ellerman K;
A, Khramtsov NV;
A, Millet I;
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Best Local S
Matches 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel isolated polypeptides, mature forms of these, or a sequence that is at least 95 % identical to, or having one more conservative amino acid substitutions in the polypeptides. The polypeptides, nucleic acid molecules and antibodies are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The nucleic acid molecules, polypeptides and antibodies are useful for treating, preventing or diagnosing diseases such metabolic disorders, diabetes, preventing or diagnosing diseases such metabolic disorders, diabetes,
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247; Conser
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                NIMDLNKDGSIDFNEFLKAPYV--VHRYE
                                              RMMDLNGDGKVDLNEFLEAFRLSDLHRKE
                                                                                                                              DGMSVMDALYANKASLVAIFNIIDADNSGBITLDBFBTAIDLLVAHMPGAYSKAEMLEKC
                                                                                                                                                                               KSGKLSVSQWAFCMENILGLNLPWRSLSSNLVNIDQNGNVEYMSSFQNIRIEKPVQEAHS
                                                                                                                                                                                                                                                                                                   QLMPHFVQYISAASQTKRLSF---KQRMGIVESSALKELAVRMRDHRDELEDEFRKYDPK
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                                                                                                                                                                                                                                                                                                                                                                                                                         -----TINGSPTEHLTEHEWEQIIDILWSDPRGKNGCPPNTCRGGGCYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DTSLRAALIIONWYRGYKARLKAROHYALTIFOSIBYADBOGOMOLSTFFSFMLENYTHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENAIRAAIFIQKWYRRHQARREMQRRCNWQIFQNLEYASEQDQAELYKFFNDLIKHMPQA
                                                                                              ---TLVETLYRYRSDLEIIFNAIDTDHSGLISVEEFRAMWKLFSSHYNVHIDDSQVNKLA
                                                                                                                                                                                                                   DSGYISISHWCKVMENVTKLGLPWRLLRDKLAPGTDSQKVNYNRTLDLLDTD-VILEAEA
                                                                                                                                                                                                                                                             GTTPRFFQY
                                                                                                                                                                                                                                                                                                                                           GPDVTSKILNKYQLKMLIRSHECKPEGYEICHDGKVVTIPSASNYYEEGSNRGAYIKLCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KYKLHGKRILQILEEFYAWLPTETNRDHGTDSKHNKVGVTFNA----
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                                                                                                                                                                                                                                                           ----QVTKATCFQPLRORVDTMENSÄIKILRERVISRKSDLTRAFQLQDHR
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Pred. No. 1.5e-100;
5; Mismatches 200;
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7;

Indels Length

67;

13

-----LGSVLNSRVLIVHGGFSDSTSLDL

251

191 177 132 117 73

-HGRIK-----

339 299

456

402

518 515 458

602

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15-NOV-2001

16-NOV-2001

20-NOV-2001

20-NOV-2001

21-NOV-2001

22-NOV-2001

22-NOV-2001

23-NOV-2001

30-NOV-2001

30-NOV-2001

30-NOV-2001

10-DEC-2001

10-DEC-2001

11-DEC-2001

11-DEC-2001

11-DEC-2001

11-DEC-2001

11-DEC-2001

11-EBB-2002

04-FEB-2002

04-FEB-2002

04-FEB-2002

04-FEB-2002

04-FEB-2002

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04-FEB-2002

05-MAR-2002

13-MAR-2002

13-MAR-2002

13-MAR-2002

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13-MAR-2002

11-MAR-2002

11-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neuroprotective; antiparkinsonian; anticonvulsant; osteopathic; antiarthritic; antiinflammatory; dermatological; antiasthmatica; antilipemic; gene therapy; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer; cardiovascular disease; infectious disease; anorexia; cancer; cardiovascular disease; hypertension; atherosclerosis; neurodegenerative disorder; hypertension; atherosclerosis; neurodegenerative disorder; osteoparthritis; hematopoietic disorder; epilepsy; immune disorder; osteoparthritis; hematopoietic disorder; inflammatory skin disorder; asthma; dyslipidemia; neurogenesis; cell differentiation; cell proliferation; hematopoiesis; wound healing; angiogenesis; chromosome mapping; tissue typing; pharmacogenomic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADJ95098 standard; protein; 613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antidiabetic; anorectic; cardiant; hypotensive; antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide; protozoacide; nootropi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel NOVX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-MAY-2004 (first
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               2001US-033561DP.
2001US-033163LP.
2001US-033163LP.
2001US-033163LP.
2001US-033341DP.
2001US-033402TP.
2001US-033452EP.
2001US-033452EP.
2001US-033452EP.
2001US-033452EP.
2001US-03357EP.
2001US-03357EP.
2001US-033594DP.
2002US-035328BP.
2002US-035328BP.
2002US-0354393P.
2002US-0354393P.
2002US-0354393P.
2002US-0354393P.
2002US-0361823P.
2002US-0361823P.
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2002US-0361823P.
2002US-036418BP.
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NRLHPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLLVVLHKNGLPS

177 132

191

- ILHAHYVLEVLFETKKVLKQMPNPTHIQTSPSKEVTICGDLHGKLDDLFLIFYKNGLPS

문 S 닭

74

14 w

TSLRAALIIQNWYRGYXARLXARQHYALTIFQSIBYADBQGQMQLSTFFSFMLBNYTHI 73

ENAIRAAIFIQKWYRRHQARREMQRRCNWQIFQNLEYASEQDQAELYKFFNDLIKHMPQA

AGRKNQYQGSAHVSVLDDKD--DLVB--EFGDIVNA-KIBLPIRKNHIDLLIDVFRKKRG

HKEELELRNQSLESEQDMRDRWDYVDSIDVPDSYNGPRLQFPLTCTDIDLLLEAPKEQQ-

Query Match
Best Local Similarity
Matches 247; Conserv

Conservative 115;

33.8%; Score 1164.5; 39.3%; Pred. No. 1.5e tive 115; Mismatches

5; DB 7;

613; 67,

Indels Length

Gaps

62

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cc human disease, preferably a NOVX-associated disorder. The nucleic acid condecules, polypeptides and antibodies are useful for treating, cc preventing or diagnosing diseases such metabolic disorders, diabetes, cobesity, infectious diseases (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer, cardiovascular diseases (hypertension, cc atherosclerosis), neurodegenerative disorders, Alzheimer's disease, epilepsy, immune disorders (osteoarthritis), cc hematopoietic disorders, inflammatory skin disorders, asthma, and various cd dyslipidemias. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, cc hematopoiesis, wound healing and angiogenesis, in gene therapy, in cc generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or diagnostic methods. The nucleic acids are further used as hybridization probes, in chromosome mapping, tissue ctyping, preventive medicine, and pharmacogenomics. This sequence corresponds to one of the NoVX polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-AUG-2002)
07-AUG-2002)
07-AUG-2002)
15-AUG-2002)
20-AUG-2002)
23-AUG-2002)
23-AUG-2002)
23-AUG-2002)
23-AUG-2002)
24-AUG-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to novel isolated polypeptides, mature forms of these, or a sequence that is at least 95 % identical to, or having one or more conservative amino acid substitutions in the polypeptides. The polypeptides, nucleic acid molecules and antibodies are useful in the manufacture of a medicament for treating a syndrome associated with a human filter of a medicament for treating a syndrome associated with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agee ML, Alsobrook JP, Berghs C, Boldog FL, Burgess CE, Chant JS Chaudhuri A, Dipippo VA, Edinger SR, Eisen A, Ellerman K; Gangolli EA, Gorman L, Gerlach VL, Ji W, Kekuda R, Khramtsov NV; Li L, Malyankar UM, Macdougall JR, Mezes PS, Miller CE, Millet I Coi CE, Ort T, Padigaru M, Patturajan M, Rastelli L, Rieger DK; Rothenberg ME, Shenoy SG, Spaderna SK, Spytek KA, Taupier RJ; Vernet CAM, Zerhusen BD, Zhong M;
Sequence 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ADJ95097.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           asthma, or infections.
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2002US-0401594P
2002US-0401787P
2002US-0403619P
2002US-0405481P
2002US-0405481P
2002US-0405492P
2002US-0405496P
2002US-0406135P
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  WPI; 2004-180133/17
                                                                                                                                                                                                                                                                                                 05-NOV-2001; 2001US-00985678
                                                                                                                                                                                                                                                                                                                        06-MAY-1999;
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                                                                                                                                                                                                                     ZHOU Y.
                                                                                                                                 ZHOU Y.
KOVALIC D K.
SCREEN S B.
TABASKA J B.
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                                                                                                          CAO
                                                  Zhou Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RMMDLNGDGKVDLNEFLEAFRLSDLHRKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGMSVMDALYANKASLVAIFNIIDADNSGEITLDEFETAIDLLVAHMPGAYSKAEMLEKC 575
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The invention describes a recombinant DNA construct comprising a colynucleotide consisting of a sequence encoding an amino acid sequence cavailable in electronic form from the US patent office at ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide cof the invention are also useful in physical arrays of molecules and as comproving plant tolerance to cold, heat, drought, herbicides, extreme commotic conditions, pathogens or pests, for manipulating growth rate in commotic conditions, pathogens or pests, for manipulating growth rate in colls by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, complant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake corress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert colypeptide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 61206; 15pp; English.
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Best Query Match Sequence 488 Local al Similarity 127; Conserv 16.9%; ilarity 41.4%; Conservative 4 8 Score 581; DB 8; Pred. No. 2.1e-45; 7; Mismatches 109 Length 488

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109;

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                                                                                                                                                                                                                                                                                                                                                                                             105 IDLLIDVFRKKRGNRLHPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLD 164
KPDIVTF 466
                                                                   VTKKFLQENNLDLI VRSHEVKDEGHEI EHDGKLI TVFSAPNYCDQMGNKGAFIRFTAPEM
                                                                                                    VTDNFLQRHRLSYVIRSHBCKPNGHBFMHDNKIITIFSASNYYAIGSNKGAYIRLN-NQL
                                                                                                                                          IRSIDR-----FCEPP-----BEGLMCELLWSDPQPQLGRGPSK-RGVALSFGAD
                                                                                                                                                                          IKSIDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMGCVPNTLRGAGVWFGPD
                                                                                                                                                                                                               MNKIYGFEGEVRSKLGEKFVELFA---EVFCWLPLAHVINNKVFVVHGGLFSVDGVKLSD
                                                                                                                                                                                                                                  MNARYGFIREVESKYPRNHKRILAFIDEVYRWLFLGSVLNSRVLIVHGG-FS-DSTSLDL
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ABB63840 standard; protein; 520 AA

26-MAR-2002 (first entry

Drosophila melanogaster polypeptide SEQ ID NO 18312

RESULT 8
ABB63840
ID ABB6
XX
AC ABB6
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AC ABB6
XX
DT 26-M
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DT Dros
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KW Dros
KW Dros
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CS Dros
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OS Dros pharmaceutical Drosophila; developmental biology; cell signalling; insecticide,

Drosophila melanogaster

WO200171042-A2

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Best Local Simi
Matches 136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 520 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 18312; 21pp + Sequence Listing; English
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genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2000; 2000US-0191637P
11-JUL-2000; 2000US-00614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WIPO at ftp.wipo.int/pub/published_pct_sequences
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DB; ABL07943.
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                                                                                                                                                                                                                                                               NIFEINGLESEKNEYLENGDEVDRGSESVECIFTLEGEKLLYENHEFILARGNHESINMNQ
YKSF 498
                                FVQY 408
                                                                                                                                                                                                 MYGFTGEVTAKYT---SAMADIFTQVFNWLPLCHCINQKILVMHGGLFSTEDVTLDHIRR
                                                                                                                                                                                                                                RYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGF--SDSTSLDLIKS
                                                                                                                                                                                                                                                                                                 VVLHKNGLPSSSNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNA
                                                                                                                                                                                                                                                                                                                                                                LIDVFRKKRGNRLHPKYVALILRBAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAVKADPAYLKGYYRRAAAHMSLGKFKQALCDFEFVAKCR-PNDKDAKLKFTECNKIVKM
                                                                 KFCKDNNLDYIIRSHEVKDMGYEVAHNGKCITVFSAPNYCDTMGNMGAFITITGNNLKPN
                                                                                             NFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRL-NNQLMPH
                                                                                                                                 IERN----CQPP--
                                                                                                                                                              IDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMGCVPNTLRGAGVWFGPDVTD
                                                                                                                                                                                                                                                                                                                               LMEHYKAQK--RLHRKFAYKILCBIDTYMRAQPSLVDITVPDEEKFTICGDIHGQFYDLM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 577; DB 4;
; Pred. No. 5.5e-45;
83; Mismatches 153
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                                                                                                                               EEGLMCELLWSDPQQWMG-LGQSKRGVGIQFGPDV
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RESULT 9

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155 AIAGDEHKRSVVDSLDIESMTIEDEYSXPKLEDGKVTISFMKE----LMQWYKDQK--KL QYQGSAHV-SVLDDKD----DLVEBFG--DIVNAKIBLPIRKNHIDLLIDVFRKKRGNRL

120 154

FIQKWYRRHQARREMOR-RCNWQIFQNLEYAS--EQDQAELYKFFNDLIKHMPQAAGRKN 67 YIMGYYRRAASNMALGKFRAALRDYETVVKVKPHDKDAKMKYQECNKIVK--PKAFER--

Query Match Best Local Sim Matches 143;

Local Similarity

16.6%;

Conservative

73;

Score 571; DB 4; Pred. No. 1.9e-44; 3; Mismatches 153

4; Length 500; Indels

42;

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ABG09989

ABG00

XX

ABG0

ABG0

XX

ABG0

                                                                                                                                        CC sequences. (I) is useful as hybridisation probes, polymerase chain of reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed (CC genes. (I) is useful in gene therapy techniques to restore normal (CC activity of (II) or to treat disease states involving (II). (II) is compared to the sequence tags for identifying expressed (CC genes. (I) is useful in gene therapy techniques to restore normal (CC suseful for generating antibodies against it, detecting or quantitating a (CC polypeptide in tissue, as molecular weight markers and as a food (CC supplement. (II) and its binding partners are useful in medical imaging (CC sites expressing (II), (II) and (II) are useful for treating disorders (CC involving aberrant protein expression or biological activity. The (CC diagnostics forensics, gene mapping, identification of mutations (CC and to produce other types of data and products dependent on DNA and (CC amino acid sequences ABG00010-ABG30377 represent novel human diagnostic camino acid sequences of the invention. Note: The sequence data for this case and to produce the printed specification, but was obtained in the printed specification, but was obtained in
                                                                patent did not appear in the printed specification, electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ ID NO 40348; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-639362/73.
N-PSDB; AAS74176.
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23-AUG-2000; 2000US-00649167.
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Sequence 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isolated polynucleotide (I) and polypeptide (II)
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RESULT 10
ABG70122
ID ABG70122
AC ABG70
XX AC ABG70
XX PREY
DT 21-0(
DT 21-0(
DX PREY
WW Bhig
XX PREY
WW PROT
XX Home

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The invention relates to a complex of protein-protein interactions Co between a Shigella flexmeri polypeptide (e.g. ospB, ospD1, ipaD, ipaC, ipaH), 8, ospG and ospG1) and a mammalian polypeptide defined in the specification. The complexes are formed using the yeast two-hybrid system. Also included are (1) a recombinant host cell expressing the interactions between the Shigella flexmeri polypeptide and a mammalian coplypeptide defined in the specification; (2) selecting a modulating compound obtained from the method of (2); (4) a SID compound that inhibits or activates the protein-protein interactions; (3) a modulating compound obtained from the method of (2); (4) a SID compound cotted interacting domain polypeptide or its fragment or variant comprising the human polypeptides appearing as ABG70042-ABG70242; (5) a Comprising the human polypeptides appearing as ABG70042-ABG70242; (5) a polypucleotide or its fragment or variant comprising the vector; and (10) a protein chip comprising Shigella containing the vector; and (10) a protein chip comprising Shigella containing the vector; and (10) a protein chip comprising Shigella containing the vector; and (10) a protein chip comprising Shigella containing the vector; and (10) a protein chip comprising Shigella containing the vector; and (10) a protein chip comprising Shigella containing the vector are set of the containing Shigella containing the vector are set of the containing Shigella containing the vector comprising Shigella containing the vector are set of the containing Shigella containing the vector and containing the vector comprising Shigella containing the vector comprising the vector compris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New complex of protein-protein interactions between a bait Shigella flexneri polypeptide and a prey mammalian or human placenta polypeptide for treating or preventing bacillary dysentery in a mammal or human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-599706/64.
N-PSDB; ABS51515.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG70122 standard; protein; 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Page 90-91; 162pp; English.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specification. A pharmaceutical composition comprising the compound, polypeptide or polymucleotide is useful for treating or preventing shigellosis (bacillary dysentery) in a human or mammal. The present sequence represents a human prey protein isolated by the yeast two-hybrid assay, forming a complex of the invention with a shigella protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 494
468 FHQF 471
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                                                            AFLEENNIDYIIRSHEVKAEGYEVAHGGRCVTVFSAPNYCDQMGNKASYIHLQGSDLRPQ
                                                                                         NFLQRHRLSYVIRSHECKPNGHBFMHDNKIITIFSASNYYAIGSNKGAYIRL-NNQLMPH
                                                                                                                                                                                                                RYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGF--SDSTSLDLIKS
                                                                                                                                                                                                                                                                 VVI.HKNGLPSSSNPYVFNGDFVDRGKRGLEVI.LLLSLYLAFPNAVFLNRGNHEDSVMNA
                                                                                                                                                                                                                                                                                                                           YIKGYYRRAASNMALGK-----FR----AALRD-----YETVVKVKPHDKDAKMKYQ
                              FVQY 408
                                                                                                                                                   IDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMGCVPNTLRGAGVWFGPDVTD
                                                                                                                                                                                 IYGFEGEVKAKYT---AQMYELFSEVFEWLPLAQCINGKVLIMHGGLFSEDGVTLDDIRK
                                                                                                                                                                                                                                              NIFELNGLESETNEYIFNGDEVDRGSESVEVILTLEGEKLLYEDHEHLLRGNHETDNMNQ
                                                                                                                                                                                                                                                                                                           LMQWYKDQK--KLHRKCAYQILVQVKEVLSKLSTLVETTLKETEKITVCGDTHGQFYDLL
                                                                                                                                                                                                                                                                                                                                                                        BCNKIVKOKAFERAIAGDEHKRSVVDSLDIESMTIEDEYSGPKLEDGKVTISFMKE----
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33.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 570; DB 5;
Pred. No. 2.3e-44;
71; Mismatches 142
                                                                                                                        CDLLWSDPOPONG-RSISKRGVSCOFGPDVTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 494;
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## AAE09722 standard; protein;

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AABO9722
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XX AABO9722
AC AABO9
XX CABO
DT 29-NC
XX CB1
XX CB1
XX Gene
XX Unide
XX Uni 29-NOV-2001 (first entry)

Novel cell cycle protein, protein phosphatase type 5 (PP5).

gene cycle protein; DNA repair; protein phosphatase type 5; PP5; therapy; cancer; vaccine; cytostatic; vulnerary; antiinflammatory.

Unidentified

Misc-difference Location/Qualifiers occurs /note= "Bncoded by CGAG; The while decoding with

exception

02-MAR-2001; 2001WO-US006849 VQ200164913-A2 This translation th AAD16789"

02-MAR-2000; 2000US-00517779

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The patent discloses cell cycle proteins and nucleic acids encoding them.
The cell cycle proteins are capable of promoting cell cycle progression
or cell cycle arrest. They are capable of promoting or inhibiting DNA
crepair. The invention also provides methods for screening a bloactive
egent capable of modulating the cell cycle or interfering with the
cc binding of a cell cycle protein, protein phosphatase type 5 (PPS). The
method involves combining a cell cycle protein and a candidate bloactive
egent and determining the effect on the cell in the presence or absence
cc agent and determining the effect on the cell in the presence or absence
cc of the candidate agent. Cell cycle proteins bind to Rad9 proteins. They
care useful for generating an agonist and antagonist of the cell cycle
cc proteins, both of which are useful in gene therapy and in screen assays.
cc They are useful in the diagnosis and treatment of cancer. The proteins of
cc the invention are used as vaccines. They are useful for generating
cc polyclonal or monoclonal antibodies to the proteins. The present sequence
is a novel cell cycle protein, protein phosphatase type 5 (PPS) of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell cycle protein having phosphatase activity for generating agonist and antagonist e.g. antibodies of the polypeptides, both of which are useful in gene therapy and in screen assays.
                    ADE64103 standard; protein; 499 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-557775/62.
N-PSDB; AAD16789, AAD16790.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 2; 75pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 FIQKWYRRHQARREMQRRCNWQIFQNLEYASEQDQAELYKFFNDLIKHMPQAAGRKNQYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 16.6%; Score 570; DB 4; I
Similarity 33.7%; Pred. No. 2.4e-44;
43; Conservative 71; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIFELNGLPSETNPYIFNGDFVDRGSFSVEVILTLFGFKLLYPDHFHLLRGNHETDNMNQ
                                                                                                                                                                                                                                                                                                                                                                                                              RYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGF--SDSTSLDLIKS
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                                                                                                                                                                         FVQY 408
                                                                                                                                                                                                               AFLEENNLDY I I RSHEVKAEGY EVAHGGR CVTVFSAPNY CDQMGNKASY I HLQGSDLRPQ
                                                                                                                                                                                                                                                                                                                                           IDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMGCVPNTLRGAGVWFGPDVTD
                                                                                                                                                                                                                                                                                                                                                                                      IYGFEGEVKAKYT---AQMYELFSEVFEWLPLAQCINGKVLIMHGGLFSEDGVTLDDIRK 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LMOWYKDOK--KLHRKCAYQILVQVKEVLSKLSTLVETTLKETEKITVCGDTHGQFYDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIDVFRKKRGNRLHPKYVALILRBAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------GSAHV-SVLDDKD----DLVEBFG--DIVNAKIELPIRKNHIDL
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                                                                                                                                                                                                                                                                                                   DSGPM-----CDLLWSDPQPQNG-RSISKRGVSCQFGPDVTK
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11 FIQKWYRRHQARREMQRRCNWQIFQNLEYASBQDQABLYKFFNDLIKHMPQAAGRKNQYQ 70

Mismatches

Indels

68;

Gaps

16

-FR---

AALRD----YETVVKVKPHDKDAKMKYQ

Local Similarity

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Query Match
Best Local S
Matches 143
                                                                                                                                 comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a control of the perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal control of the expression of a polynucleotide sequence which is differentially expression of a polynucleotide sequence which is differentially considered to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound for identifying a compound or small molecule that regulates the activity of one or more of the composition, a method for identifying a pharmaceutical compound useful in treating activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more compound that the compound of the polypeptides or their antibodies. The polymucleotide or the compound that conjury (CCI) and spared nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene the sequence data for this patent did not form part of the printed of the specification, which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed at the patent did not form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or human polynucleotides or a polynucleotide which represents a fragme derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human;
spinal
                                                                               Sequence 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New composition comprising two or more isolated polypeptides, useful preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention discloses a composition comprising two or more isolated rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-268312/26
GENBANK; P53041.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GEHO)
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                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pain; neuronal tissue; gene therapy;
segmental nerve injury; chronic constriction injury; CCI;
nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEN HOSPITAL CORP.
BAYER AG.
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                    16.6%;
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                  Score 570; DB 7;
Pred. No. 2.4e-44;
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                               tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe;
                                                                          New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
                                                                                                                                                                             Wu I'D,
                                                                                                                                                                                                                                   02-OCT-2002; 2002US-0414971P
                                                                                                                                                                                                                                                             29-SEP-2003; 2003WO-US028547.
                                                                                                                                                                                                                                                                                         15-APR-2004.
                                                                                                                                                                                                                                                                                                                   WO2004030615-A2
                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                  chromosome identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumour-associated antigenic target; TAT; human; overexpression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour-associated antigenic target (TAT) polypeptide PRO25881, SEQ:5498
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                                                                                                                                                                                                        GENENTECH INC.
                                                                                                                                                                           Zhang
                                                                                                                                      ACN40614.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRL-NNQLMPH 404
                                                                   cancer or tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FHQF 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGF--SDSTSLDLIKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IYGFEGEVKAKYT----AQMYELFSEVFEWLPLAQCINGKVLIMHGGLFSEDGVTLDDIRK 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LMQWYKDQK--KLHRKCAYQILVQVKEVLSKLSTLVETTLKETEKITVCGDTHGQFYDLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ECNKIVKQKAFERAIAGDEHKRSVVDSLDIESMTIEDEYSGPKLEDGKVTISFMKE----
                                        SEQ
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                                                                                                                                                                                                                                                                                                                                                                      cytostatic.
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                                     7273pp;
                                                                                                                                                                                                                                                                                                                                                                                  chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----CDLLWSDPQPQNG-RSISKRGVSCQFGPDVTK
                                     English
                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer;
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The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are

RESULT 14
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ID ADB64
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AC ADE64
XX
DT 29-JA
DT 29-JA
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KW Rat F
KW Rat;
KW Chror
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Rattu

Rat Protein 29-JAN-2004

P53042,

SEQ ID NO 10049

(first

entry)

ADE64101 standard; protein;

499

Rattus norvegicus

Rat; pain; chronic co

constriction

neuronal tissue; gene therapy; spinal segmental nerve injury; nstriction injury; CCI; spared nerve injury; SNI; Chung.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and cold; an antibody specific for a TAT polypeptide; acid; an antibody specific for a TAT polypeptide; for the treatment or cancer which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorretal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local (
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473
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                                        FVQY 408
                                                                                AFLEENNLDYIIRSHEVKAEGYEVAHGGRCVTVFSAPNYCDQMGNKASYIHLQGSDLRPQ 472
                                                                                                                       NFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRL-NNQLMPH
                                                                                                                                                                                                              IDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMGCVPNTLRGAGVWFGPDVTD
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Pred. No. 2.4e-44;
1; Mismatches 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention discloses a composition comprising two or more isolated rat CC or human polynucleotides or a polynucleotide which represents a fragment, CC derivative or allelic variation of the nucleic acid sequence. Also CC claimed are a vector comprising the nucleotide a host cell comprising the vector, a method for identifying a nucleotide sequence kit to perform the method, an array, a method for identifying an agent ckit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence cc that is differentially expressed in neuronal tissue of a first animal cc subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a compound that regulates the activity of one or more of the specification, a method for identifying a compound useful in treating complypeptides or their antibodies. The polynucleotide given in the cativity in an animal of one or more of the polynucleotide or the compound that composition comprising the one or more complypeptides or their antibodies. The polynucleotide or the compound that composition comprising the one or more compound useful in treating compound that sactivity is useful for preparing a medicament for treating compound that sactivity is useful for preparing a medicament for treating compound that sactivity is useful for preparing a medicament for treating compound useful in treating compound that sactivity is useful for preparing a medicament for treating compound that sactivity is useful for preparing a medicament for treating compound that sactivity is useful for preparing a medicament for treating compound that sactivity is useful for preparing a medicament for treating compound that sactivity is useful for preparing a medicament for treating compound that sactivity is useful for preparing a m
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(FARB )
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26-NOV-2001; 2001US-0333347P.
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                                            VVLHKNGLPSSSNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNA
                                                                                                                                  LIDVFRKKRGNRLHPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLL
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                                                                                     LMQWYKDQK--KLHRKCAYQILVQVKSVLCKLSTLVETTLKETEKITVCGDTHGQFYDLL
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EMORRCNWQIFQNLEYASEQDQAELYKFFNDLIKHMPQAAGRKNQYQGSAHVSVLDDKDD 83

-VEVEPQYAGARIE---

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Query Match Best Local S Matches 139

Local Similarity

Conservative

16.3%; Score 562.5; DB 5; 35.8%; Pred. No. 1.1e-43; tive 55; Mismatches 125;

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                                                         The patent discloses nucleotide sequences derived from a plant genome, encoding polypeptides which can be activated as signalling molecules in the signal transduction pathway of plant pathogen resistance, which results from interaction between polypeptide products of a resistance gene and elicitors encoded by an avirulence gene in the pathogen and the protest interacts with the product of the resistance gene. The sequences of the invention are used to activate defence mechanisms against plant pathogens in plants. The present sequence is tomato interactor S-25 (PPS, tetratricopeptide (TPR)-phosphatase) protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequences derived from plant genome and encoding polypeptides which interact with the product of a resistance gene are involved in signal transduction and are useful to activate plant defense against a pathogen.
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             The patent discloses nucleotide sequences derived from a plant genome, encoding polypeptides which can be activated as signalling molecules in the signal transduction pathway of plant pathogen resistance, which results from interaction between polypeptide products of a resistance gene and elicitors encoded by an avirulence gene in the pathogen and the protein interacts with the product of the resistance gene. The sequences of the invention are used to activate defence mechanisms against plant pathogens in plants. The present sequence is tomato interactor S-25 (PPS, pathogens in plants. The present sequence is tomato interactor S-25 (PPS,
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(TPR) -phosphatase)
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RESULT 17
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Matches
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Cell cycle protein having phosphatase activity for generating antagonist e.g. antibodies of the polypeptides, both of which in gene therapy and in screen assays.
                                              WPI; 2001-557775/62.
                                                                                                               02-MAR-2000; 2000US-00517779
                                                                                                                                      02-MAR-2001;
                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                            mutant; mutein;
                                                                                                                                                                                                                                                                                                                          Protein phosphatase
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                                                                                                                                                                                                                                                                                        cycle protein; DNA repair; protein phosphatase type 5; therapy; cancer; vaccine; cytostatic; vulnerary; antiir
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                                                                                         RIGEL
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                                                                                                                                                                                                                   Location/Qualifiers 303
                                                                                                                                                                                                                                                                             variant.
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                                                                                                                                                                                                                                                                                                                                                                                              protein;
                                                                                         INC
                                                                                                                                                                                                                                                                                                                         type 5
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35.8%; Pred. No. 1.2e-43;
tive 55; Mismatches 125
                                                                                                                                                                                                        "Wild-type Asn
                                                                                                                                                                                                                                                                                                                          (PP5) variant, N303A.
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are useful
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Claim 16; Page; 75pp; English

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RESULT 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The patent discloses cell cycle proteins and nucleic acids encoding them.

CT The cell cycle proteins are capable of promoting cell cycle progression

CT or cell cycle arrest. They are capable of promoting or inhibiting DNA

CT repair. The invention also provides methods for screening a bloactive

CT agent capable of modulating the cell cycle or interfering with the

CT binding of a cell cycle protein, protein phosphatase type 5 (PPS). The

CT method involves combining a cell cycle protein and a candidate bloactive

CT agent and determining the effect on the cell in the presence or absence

CT agent and determining an agonist and antagonist of the cell cycle

CT are useful for generating an agonist and antagonist of the cell cycle

CT proteins, both of which are useful in gene therapy and in screen assays.

CT they are useful in the diagnosis and treatment of cancer. The proteins of

CT the invention are used as vaccines. They are useful for generating

CT polyclonal or monoclonal antibodies to the protein, protein phosphatase type

CT is N303A variant of a novel cell cycle protein, protein phosphatase type

CT consideration but it desired from the present sequence is not shown in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Simi
Matches 142;
Cell cycle protein; DNA repair; protein phosphatase type 5; PP5; gene therapy; cancer; vaccine; cytostatic; vulnerary; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 499 AA;
                                                                 Protein phosphatase type 5 (PP5) variant, H244A.
                                                                                                              29-NOV-2001
                                                                                                                                                                                                 AAE09731 standard; protein; 499 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specification, but is derived from the PP5 protein shown in Fig 2
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                                                                                                                                                                                                                                                                                                              473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      312 IYGFEGEVKAKYT---AQMYELFSEVFEWLPLAQCINGKVLIMHGGLFSEDGVTLDDIRK 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VVLHKNGLPSSSNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YIKGYYRRAASNMALGK-----PR----AALRD-----YETVVKVKPHDKDAKMKYQ
                                                                                                                                                                                                                                                                                                                                                                                               AFLEENNLDYIIRSHEVKAEGYEVAHGGRCVTVFSAPNYCDQMGNKASYIHLQGSDLRPQ 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IERNR-----QPP--DSGPM-----CDLLWSDPQPQNG-RSISKRGVSCQFGPDVTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGF--SDSTSLDLIKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIDVFRKKRGNRLHPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The patent discloses cell cycle proteins and nucleic acids encoding them. CC The cell cycle proteins are capable of promoting cell cycle progression or cell cycle arrest. They are capable of promoting or inhibiting DNA repair. The invention also provides methods for screening a bioactive agent capable of modulating the cell cycle or interfering with the binding of a cell cycle protein phosphatase type 5 (PPS). The method involves combining a cell cycle protein and a candidate bioactive agent and determining the effect on the cell in the presence or absence of the candidate agent. Cell cycle proteins bind to Rad9 proteins. They are useful for generating an agonist and antagonist of the cell cycle proteins, both of which are useful in generating an agonist and antagonist of ancer. The proteins of the invention are used as vaccines. They are useful for generating of the invention are used as vaccines. They are useful for generating of the invention anough cell cycle protein, protein phosphatase type CC is H244A variant of a novel cell cycle protein, protein phosphatase type CC is protein, but is derived from the PPS protein shown in Fig 2
                                                                                                                                                                                                                                                                                                                                                        Matches 142;
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 499
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                                                                                                                                                                                                                                                                                                             11 FIQKWYRRHQARREMORRCNWQIFQNLEYASEQDQAELYKFFNDLIKHMPQAAGRKNQYQ
RYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGF--SDSTSLDLIKS
                                    NIFELNGLPSETNPYIFNGDFVDRGSFSVEVILTLFGFKLLYPDHFHLLRGNHETDNMNQ
                                                                                                                                                    LIDVFRKKRGNRLHPKYVALILRBAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLL
                                                                                                                                                                                               ECNKIVKQKAFERAIAGDEHKRSVVDSLDIESMTIEDEYSGPKLEDGKVTISFMKE----
                                                                         VVLHKNGLPSSSNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNA
                                                                                                                  LMQWYKDQK--KLHRKCAYQILVQVKEVLSKLSTLVETTLKETEKITVCGDTAGQFYDLL
                                                                                                                                                                                                                                -----GSAHV-SYLDDKD----DLVEEFG--DIVNAKIELPIRKNHIDL 107
                                                                                                                                                                                                                                                                           YIKGYYRRAASNMALGK-----FR----AALRD-----YETVVKVKPHDKDAKMKYQ
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33.5%;
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Pred. No. 2.1e-43;
                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                           Length 499;
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IYGFEGEVKAKYT---AQMYELFSEVFEWLPLAQCINGKVLIMHGGLFSEDGVTLDDIRK 368

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RESULT 19
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                                                   The patent discloses cell cycle proteins and nucleic acids encoding them.

Common the cell cycle proteins are capable of promoting cell cycle progression or cell cycle arrest. They are capable of promoting or inhibiting DNA compatitions are capable of promoting or inhibiting DNA compatitions. The invention also provides methods for screening with the compatition of a cell cycle protein phosphatase type 5 (PP5). The compatition of a cell cycle protein phosphatase type 5 (PP5). The compatition of a cell cycle protein and a candidate bioactive method involves combining a cell cycle protein and a candidate bioactive compatition of the candidate agent. Cell cycle protein and a candidate bioactive compatition and determining the effect on the cell in the presence or absence compatition and agents. Cell cycle proteins bind to Rad9 proteins. They care useful for generating an agonist and antagonist of the cell cycle proteins, both of which are useful in gene therapy and in screen assays. Compatition are useful in the diagnosis and treatment of cancer. The proteins of the invention are used as vaccines. They are useful for generating compatition are used as vaccines. They are useful for generating compatition are useful cycle protein, protein phosphatase to the protein phosphatase to the protein some phosphatase compatition and the capacitic phosphatase to the protein some phosphatase that the capacitic phosphat
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gene therapy; cancer; vaccine; cytostatic; vulnerary; antiinflammatory;
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                                           type 5 (PP5) of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nitrogen;
bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; pathogen tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; homologous recombination; seed oil yield; protein yield; carbohydrate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                               (SLAT/)
                                                                                          (CAOY/)
                                                                                                                                                                                                                                                                                                             18-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADS44165 standard; protein; 473
                                                                                                                                                                                     21-FEB-2002; 2002US-0360039P
                                                                                                                                                                                                                                                 20-FEB-2003; 2003US-00369493
                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADS44165
      GOLD/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 RYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGF--SDSTSLDLIKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             252 NIFBLNGLPSETNPYIFNGDFVAAGSFSVEVILTLFGFKLLYPDHFHLLRGNHETDNMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95 YIKGYYRRAASNMALGK-----FR----AALRD----YETVVKVKPHDKDAKMKYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 FIQKWYRRHOARREMORRCNWQIFQNLEYASEQDQAELYKFFNDLIKHMPQAAGRKNQYQ
HINKLE G J.
SLATER S C.
CHEN X.
GOLDMAN B S.
                                                                                                                          CAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFLEENNLDYIIRSHEVKAEGYEVAHGGRCVTVFSAPNYCDQMGNKASYIHLQGSDLRPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIDVFRKKRGNRLHPKYVALILRBAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LMQWYKDQK--KLHRKCAYQILVQVKEVLSKLSTLVETTLKETEKITVCGDTHGQFYDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phosphorus; photosynthesis; polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide #22595.
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33.3%; Pred. No. 5e-43;
tive 71; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC The invention relates to a recombinant DNA construct comprising a CC provide for expression of a polynucleotide encoding a polypeptide from a CC comprising the recombinant DNA construct and a method of producing a CC comprising the recombinant DNA construct and a method of producing a CC transformed plant having an improved property. The plant is a crop plant CC such as maize or soybean. The method of producing a transformed plant the recombinant DNA construct and growing the transformed plant with the CC recombinant DNA construct and growing the transformed plant with the CC improved plant properties and growing the transformed plant properties. CC inference to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased resistance to plant disease, better growth rate of content, improved yield by modification of protein yield and/or CC content, improved lignin production of protesynthesis or by phosphorus use and/or uptake, by modification of photosynthesis or by croviding improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan CC production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not cform part of the printed specification but was obtained in electronic CC format from USPTO at secuence at least one stress condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 473 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                   VYRWLPLGSVLNSRVLIVHGGF--SDSTSLDLIKSIDRGKYVSILRPPLTDGEPLDKTEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLLVVLHKNGLPSSSNPYVFNGDFVDRG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AHVSVLDDKDDLVBEFGDIVNAKIBLPIRKNHIDLLIDVFRKKRGNRLHPKYVALILREA 132
                                                                                                                                                                                                                             QQIFDIMWSDPQATMGCVPNTLRGAGVWFGPDVTDNFLQRHRLSYVIRSHECKPNGHEFM 370
                                                                                                                                                                                                                                                                                                                                                                   SWSTEVAFTLYAYKLLYPDAVFINRGNHETDDMNKVYGFEGECRSKY---NERTFNIFSE
                                                                                                                                    HDNKITTIFSASNYYAIGSNKGAYIRLNNQLMPHFVQY 408
                                                                                                                                                                                                                                                                        TFSLLPLGSLISDSYLVVHGGLFSDDNVTLDQLRNIDRFS----KKQPGQSG------
                                                                                                                                                                                                                                                                                                                                                                                                                 KRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNARYGFIREVESKYPRNHKRILAFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               KELLEKTPSLIDIPVKGDETLVICGDTHGQYFDLLNIFKLHGPPSPTNKYLFNGDFVDRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANINIED--MDIPSDYDGVI---LEKQITKEFVEDMKERF--CQGKKLPLKFAYSILRDL 191
                                                                                    HDGYCITVFSAPNYCDSTGNLGAVIKVKEDMELDFHQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 519; DB 8;
Pred. No. 1.5e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen X,
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Query Match Best Local S Matches 141

Local Similarity les 141; Conser

14.6%;

Pred. No. 7.9e-38;

8

Mismatches

Gaps

IQKWYRRHQARREMQRRCNWQIFQNLEYASEQDQAELYKFFNDLIKHMPQAAGRKNQYQG 71

YAAILNPKEAVKDFKTCVKIAP

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The invention relates to a recombinant DNA construct comprising a CC prowder functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a CC comprising the recombinant DNA construct and a method of producing a CC transformed plant having an improved property. The plant is a crop plant CC such as maize or soybean. The method of producing a transformed plant the recombinant DNA construct and growing the transformed plant with the CC transformed plant by construct and growing the transformed plant, where the CC plynucleotide or polypeptide is useful for improving plant with the complication of the recombinant DNA construct and growing the transformed plant, where the collynucleotide or polypeptide is useful for producing plant properties. CC The recombinant DNA construct is useful for producing plant properties. CC improved plant properties, e.g. improved cold, heat or drought tolerance, contracted to harbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification CC of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or CC content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by conduction, improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan or production. Note: The sequence data for this patent did not corm part of the printed specification but was obtained in electronic CC format from USPTO at sequence data for this patent did not corm part of the printed specification but was obtained in electronic CC format from USPTO at sequence data for this patent did not corm to the printed specification but was obtained in electronic CC forms at few parts of the corm                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant DNA construct comprising a promoter positioned to provi
for expression of a polynucleotide encoding a polypeptide from a
microbial source, useful for producing plants with improved properties.
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Sequence 598 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1;
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(SLAT/)
(CHEN/)
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SLATER S C.
CHEN X.
GOLDMAN B S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 4091; 122pp; English
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food su
                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
The invention relates to isolated polynucleotide (I) and polypeptide sequences. (I) is useful as hybridisation probes, polymerase chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome mapping; gene mapping; gene therapy; forensic;
upplement; medical imaging; diagnostic; genetic disorder.
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                                                                                             SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnostic protein #9979
                                                                                                                                                                                                                                                                                                                                                                     Liu C,
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                                                                                             IJ
                                                                                       NO 40347;
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ENNLDYITRSHEVKAEGYEVAHGGRCVTVFSAPNYCDQMGNKASYIHLQGSDLRPQFHQF
                                                                                                                  LGPVHLLHGAVMASTVVTMVRGEGTVTAEHTCPYLFNGRSISKRGVSCQFGPDVTKAFLE
                                                                                                                                                                              ----ATMGCVPNTL----
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Pred. No. 3.9e-37;
2; Mismatches 147;
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ABR53882 standard; protein; 513 B

20-JUN-2003 (first entry)

Protein sequence #SEQ ID 2629.

Multiprotein complex; eukaryote; drug target; diagnosis

Saccharomyces cerevisiae

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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to multiprotein complexes from eukaryotes. Proteins of the invention and DNA sequences encoding them are given in records ABR52568-ABR53903 and ACC66610-ACC61944 respectively. The complexes are obtainable by using a protein as a bait and isolating the set of proteins which is attached thereto from cells. Such protein complexes may comprise up to 30 distinct proteins. Protein complexes of the invention are useful for disgnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder. Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the Buropean Patent Office. The complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated protein complexes useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of disease disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 2629; 17pp +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CELL-) CELLZOME AG
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                                                                                                                                                                                                                                                                                         208
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                                                                        380
                                                                                                                                            328 YKY----SQRIFNMFAQSFESLPLATLINNDYLVMHGGLPSDPSATLSDFKNIDR-----F
429 KIFRSHELRMGGVQFEQKGKLMTVFSAPNYCDSQGNLGGVIHV 471
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                                                                                                                                                                                                                  GPKHTYLFNGDFVDRGSWSCEVALLFYCLKILHPNNFFLNRGNHESDNWNKIYGFEDECK
                                                                                           SSSNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNARYGFIREVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18
                                   YVIRSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRL 397
                                                                        AQPP-RDG--
                                                                                                                                                                           SKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGF-SD-STSLDLIKSIDRGKYVSI 294
                                                                                                                                                                                                                                                                                      YLPKKYVAAIISHADTLFROEPSMVELENNSTPDVKISVCGDTHGQFYDVLNLFRKFGKV
                                                                                                                                                                                                                                                                                                                         RIHPKYVALILRBAAKSIKQLPNISPV--STAVSQQVTVCGDIHGKIDDLLVVLHKNGLP
                                                                                                                                                                                                                                                                                                                                                             ----EGPKLEFE-----QLYDDKN-----AFKGAKIKNMSQEFISKMVNDLFLK--GK 207
                                                                                                                                                                                                                                                                                                                                                                                            MPQAAGRKNQYQGSAHVSVLDDKDDLVBEFGDIVNAKIELPIRKNHIDLLIDVFRKKRGN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                DPAATKALLTCDRFIREERFRKAIGGAENEAKISLCOTLNLSSFDANADLANY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DENAIRAAIFIQKWYRRHOARREM---QRRCNWQIFQNLEYASEQDQAELYKFFNDLIKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gavin A, G
M, Schultz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   available on CD-ROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Å,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'n,
                                                                      ----AFMELLWADPQEANGMGPSQ-RGLGHAFGPDITDRFLRNNKLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 479.5; DB 6;
Pred. No. 9.3e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Krause R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kruse UD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 51;
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RESULT 24 ADK64862

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                                                                                                                                                                                                                                                                                                                                         proteins are selected from given protein complexes, which are not defined CC in the specification. The variants are encoded by nucleic acids that the hybridize to the nucleic acids encoding the proteins under low stringency conditions. The protein complexes are useful as targets for an active useful as drugs targets for the treatment or preventing of a disease or CC disorder. The complexes and methods above are useful in disgnosing or CC for developing a disease or disorder or a predisposition CC for developing a disease or disorder in subject. These are also useful conforments of the complex is useful for the manufacture of a disease or CC disorder. The molecule that modulates the amount, activity or protein CC for the treatment or prevention of a disease or components of the complex is useful for the manufacture of a medicament CC for the treatment or prevention of a disease or disorder. This sequence CC corresponds to a protein of the invention. (Note: the sequence data for this patent did not form part of the printed specification but was considered from the EPO in electronic format).
                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 130; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New proteins and protein complexes from eukaryotes, useful as targets in drug screening, or in diagnosing or screening for the presence of a disease or disorder, or a predisposition for developing a disease or disorder in a subject.
                                                                                                                                                                                                                                                                                                           Sequence 513 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 3169; 13pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ADK64863.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein complex; drug target; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disease treating protein complex-derived protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    second protein, or its derivative, fragment, homologue or variant. The proteins are selected from given protein complexes, which are not defined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel protein complexes comprising a first and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bauer A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-DEC-2001; 2001EP-00130253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marzioch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADK64862 standard; protein; 513
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                                   RIHPKYVALILREAAKSIKQIPNISPV--STAVSQQVTVCGDIHGKIDDILVVIHKNGIP 176
YLPKKYVÄÄIISHÄDTLFRQEPSMVELENNSTPDVKISVCGDTHGQFYDVLNLFRKFGKV
                                                                                                               MPQAAGRKNQYQGSAHVSVLDDKDDLVEBFGDIVNAKIBLPIRKNHIDLLIDVFRKKRGN
                                                                                                                                                                                         DENAIRAAIFIQKWYRRHQARREM----QRRCNWQIFQNLEYASEQDQAELYKFFNDLIKH
                                                                                                                                                     DPAATKALLTCDRFIREERFRKAIGGAENEAKISLCQTLNLSSFDANADLANY-----
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M, Grandi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leutwein C,
                                                                                                                                                                                                                                 Conservative
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P, Krause R,
                                                                                                                                                                                                                                                   13.9%; Score 479.5; DB 7; 32.3%; Pred. No. 9.3e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rick J;
                                                                                                                                                                                                                               68;
                                                                                                                                                                                                                                 Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G, Kuester
Kruse U, N
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                                                                                                                                                                                                                                                                   Length 513;
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RESULT 25
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ADS43550
ADS4350
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polymucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transformed plant with the recombinant DNA construct and growing the transformed plant, where the polymucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; pathogen tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 21980; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-FEB-2002; 2002US-0360039P
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SLATER
CHEN X.
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ABB59732;
                               ABB59732 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MPQAAGRKNQYQGSAHVSVLDDKDDLVEEFGDIVNAKIELPIRKNHIDLLIDVFRKKRGN
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ID ABBS9732;
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ABBS9732;
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ABBS9732;
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Z6-MAR-2002 (first entry)
XX
DT 26-MAR-2002 (first entry)
XX

XX
Drosophila melanogaster polypeptide SEQ iD NO 5988.
XX

Drosophila; developmental biology; cell signalling; insecticide;
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XX
Drosophila melanogaster.
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XX

XX

Drosophila melanogaster.
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Drosophila melanogaster.
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PD 27-SEP-2001.
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PD 27-SEP-2001.
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23-MAR-2001; 2001WO-US009231.
XX

PR 23-MAR-2000; 2000US-00614150.
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PA (PEKE) PE CORP NY.
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                                 nitrogen;
bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL18175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                              Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; pathogen tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; interest to the protein plant growth regulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genes from Drosophila
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   Bacteria
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                                                                                                                                                                                                                                                                          ADS23974 standard; protein; 244
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                                                                                                                                                                                                                                                                                                                                                                 AKLVCHFV 309
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                                phosphorus; photosynthesis; lignin;
polypeptide.
                                                                                                                                                                      polypeptide #13007.
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Pred. No. 3.1
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Best Local Similarity
Matches 98; Conserv
                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positic provide for expression of a polynucleotide encoding a polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 13007; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
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(CHEN/)
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                                                                                                 SLDLIKSIDRGKYVSILRPPLTDGEPLDKTEWQQ--IFDIMWSDPQATMGCVPNTLRGAG
                                                                                                                                                          ETDDMNKVYGFBGBCRAKY---NETMFKVFSESFSALPLATLIGNKYLVLHGGLFSDDKT
                                                                                                                                                                                                                                                                        GKIDDLLVVIHKNGLPSSSNPYVFNGDFVDRGKRGLEVILLLISLYLAFPNAVFLNRGNH
  LQFGPDVTKRFCENNGLEAIIRSHEVRMNGYEVEHDGRCITVFSAPKYCDTTENKGAFIK
                                      VWFGPDVTDNFLQRHRLSYVIRSHECKPNGHEFWHDNKIITIFSASNYYAIGSNKGAYIR
                                                                               TLDDIRKLNRHN-----
                                                                                                                                                                                             EDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGF---SDST
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                                                                                                                                                                                                                                                                                                                                 13.1%; Score 451; DB 8; 38.1%; Pred. No. 1.4e-33;
                                                                                                                                                                                                                                                                                                                   43;
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                                                                               -QKQPGQQGLMMEMLWTDPQTEPGRGPSK-RGVG
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RESULT 28
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                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide (PPSRP). The specification describes PPSRP polypeptides designated PpP2A-1, PpPP-1, BnPP2A-1, BnPP2A-2, BnPP2A-3, GmPP2A-1, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rrotein phosphatase stress-related polypeptide; ppSRP; ppPP2A-1; ppPP-1;
BnPP2A-1; BnPP2A-2; BnPP2A-3; GmPP2A-1; GmPP2A-2; GmPP2A-3; OsPP2A-1;
OsPP2A-2; OsPP2A-3; plant tolerance; environmental stress; plant;
drought; salinity; cold; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                related to the above species, in a evolutionary and polypeptide structural studies, in determination of PPSRP regions required for function, modulation of PPSRP activity, modulation of metabolism of one or more cell functions and transmembrane transport of one or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New protein phosphatase stress-related polypeptide coding nucleic acid, useful for modulating plant's tolerance to an environmental stress such as drought, increased salinity and cold.
                                                                                                                                                                                                                                                                                                                                                             Sequence 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 13; Page 81; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bohnert HJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-SEP-2001;
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                                             standard;
FPNAVFLNRGNHEDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVL
                                                                                                                                                                                                  DIVNAKIELP-IRKNHIDLLIDVFRKKRGNRLHPKYVALILREAAKSLKQLPNISPVSTA
                                                                                                                                                  DIINRLLEVPTLPAKQVQLSESEIRQ------LCVVSREI---FLQQPNLLELEAP
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                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                             A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen R,
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31.2%;
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                                                                                                                                                                                                                                                  Score 435.5;
Pred. No. 6.4e
66; Mismatches
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polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ftp.seqdata.uspto.gov/sequence.thml?DocID:2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring
                                                                                                                                                                                                                                                                                                                                    New recombinant DNA construct, useful for improving plant tolerance cold, heat, drought, herbicides, extreme osmotic conditions, pathogo pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         recombinant DNA construct; physical array; plant breeding marker; cold clerance; heat tolerance; drought tolerance; herbicide tolerance; cruthe commotic condition; pathogen tolerance; pest tolerance; pest tolerance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant g
                                                                                                                                                                               The invention describes a recombinant DNA construct comprising polynucleotide consisting of a sequence encoding an amino acid
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(XOVA/)
                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 50385; 15pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) LIU J.
) ZHOU Y.
) KOVALIC D K.
) SCREEN S E.
) TABASKA J E.
CAO Y.
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 25-FEB-1999

05-MAR-19999

09-MAR-19999

23-MAR-19999

25-MAR-19999

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16-APR-19999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  increased resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert polypeptide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                            Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 339
                                                                                                                                                                                                                                                                         EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis
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al Similarity 30.1%; Pro
106; Conservative 72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRHTPRPSPGRK---EGGGKMMMTR-----APMGPMEGAAVDEMVRR-----LVEGGRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----PARIPDYGLLCDLLWSDPSPDGEGWGESDRGVSCTFGADKLVEFLEKNDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMGCVPNTLRGAGVWFGPDVTDNFLQRHRL
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99US-0125788P
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Pred. No. 8.7e-32;
2; Mismatches 135; Indels 39
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23-APR-1999;
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99US-0130149P
99US-0130510P
99US-0130891P
99US-0131449P
99US-0132048P
99US-0132407P
99US-0132485P
99US-0132486P
0144005P
0144085P
0144325P
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-0140695P.
-0140923P.
-0141287P.
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)139899P.
)140353P.
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143624P.
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RESULT 31
ADN72465
ID ADN72
XX ADN72
AC ADN72
XX Thale
XX Dlant
KW plant
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KW anima
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XX OS Arabi
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28-OCT-1999
28-OCT-1999
29-OCT-1999
                                                                plant; transgenic; E2Fa/DPa transcription factor; growth regulator; animal feed product; thale cress; cell wall biosynthesis; nitrogen metabolism; carbon metabolism.
                                                                                                            Thale
                      WO2004035798-A2
                                            Arabidopsis thaliana.
                                                                                                                                   15-JUL-2004
                                                                                                                                                         ADN72465;
                                                                                                                                                                            ADN72465 standard; protein;
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                                                                                                                                                                                                                                               LQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRLNNQLMPHF
                                                                                                                                                                                                                                                                                              RGKYVSILRPPLTDGBPLDKTEWQQIFDIMWSDPQATMGCVPNTLRGAGVWPGPDVTDNF
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LFEYGGFPPEAN-YLFLGDYVDRGKQSLETICLLLAYKIKYPENFFLLRGNHESASINRI
                                                                                                                                                                                                                                                                                                                                                                                                                 SGKQVH-----LSEG--EIRQLCAVSKEIFLQQPNLLELEAPIKICGDIHGQYSDLLR
                                                                                                                                                                                                                                                                                                                                                                                                                             -GNRLHPKYVALILREAAKSLKQLPNIS-----PVSTAVSQQVTVCGDLHGKLDDLLV
                                                                                                         protein upregulated
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99US-0159331P

99US-015963PP

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99US-0160767P

99US-0160768P

99US-0160814P

99US-0160815P

99US-0160815P

99US-0160815P

99US-0160981P

99US-0161981P

99US-0161405P

99US-0161405P

99US-0161359P

99US-0161359P

99US-0161350P

99US-0161393P

99US-0161930P

99US-0161930P

99US-0161933P

99US-0161933P
                                                                                                                                                                                                                                                                              ----PMDIPESGLVCDLLWSDPSGDVGWGMND-RGVSYTFGADKVAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.6%; Score 434; DB 3;
29.6%; Pred. No. 8.7e-32;
tive 68; Mismatches 120
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                                                                                                            in
                                                                                                           E2Fa/Dpa expressing plants SeqID
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99US-0144335P 99US-0144352P 99US-0144864P 99US-0145086P 99US-0145086P 99US-0145089P 99US-0145218P 99US-0147302P 99US-0147302P 99US-0147303P 99US-014972P 99US-014972P 99US-014972P 99US-014972P 99US-014972P 99US-014972P 99US-0151066P 99US-0151066P 99US-0151068P 99US-0151068P 99US-0151068P 99US-0151068P 99US-0151068P 99US-0151069P 99US-0151069P 99US-0151069P 99US-0151711P 99US-0157117P 99US-0157159 99US-0158029P 99US-0158039P 99US-0158039P 99US-0158039P 99US-0158039P 99US-0158039P 99US-0159293P 99US-0159293P 99US-0159293P 99US-0159293P

16-AUG-1999; 17-AUG-1999; 18-AUG-1999; 20-AUG-1999;

20-AUG-1999; 20-AUG-1999; 23-AUG-1999; 23-AUG-1999;

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22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999;

19-JUL-1999 20-JUL-1999 20-JUL-1999 20-JUL-1999 20-JUL-1999 21-JUL-1999 21-JUL-1999 21-JUL-1999

25-AUG-1999 26-AUG-1999 27-AUG-1999 27-AUG-1999 30-AUG-1999 31-AUG-1999 31-AUG-1999 31-SEP-1999 11-SEP-1999 15-SEP-1999 16-SEP-1999 16-SEP-1999 22-SEP-1999 22-SEP-1999 23-SEP-1999 24-SEP-1999 24-SEP-1999 25-OCT-1999 07-OCT-1999 08-OCT-1999 08-OCT-1999 11-OCT-1999 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up or down-regulated in transgenic plants overexpressing the heterodimeric E2Fa/DPa transcription factor of Arabidopsis and using these sequences to alter plant characteristics accordingly. The present invention describes generating transgenic plants for the production of growth regulators, can make the products of the present invention describes of enzymes, therapeutics, pharmaceuticals and animal feed products, where the altered plant characteristics are selected from increased yield or blomass, enhanced survival capacity, stress tolerance, plant architecture or physiology, altered endoreduplication, blochemistry, signal transduction, storage lipid mobilisation and/or altered photosynthesis, each relative to the corresponding wild type plants. Accordingly, these sequences can also be useful as positive or negative selectable markers can also be useful as positive or negative selectable markers during transformation of cells or tissues. The identified genes play a cole in a variety of biological processes such as DNA replication, cell wall blosynthesis, nitrogen and/or carbon metabolism or they function as transcription factors. This polypeptide sequence is thale cress protein expressed by a gene upregulated 1.3 fold or more in plants overexpressing the nearest protein are protein and protein and plants overexpressing the nearest protein are selectable markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Sir
Matches 106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 318
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                                                                                                                                                                                                                                                                                                        VLHKNGLPSSSNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MPQAAGRKNQYQGSAHVSVLDDKDDLVEEFGDIVNAKIELPIRKNHIDLLIDVFRKKR--
                                                                                                                                                                                                                                                                                                                                                                                                                 -GNRLHPKYVALILREAAKSLKQLPNIS-----PVSTAVSQQVTVCGDLHGKLDDLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAEKPAQEQEQKRAMEPAVLD------DIIRRLVE-----FRVTRPG
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LEXHDMDLICRAHQVVBDGYEFFAERQLVTVFSAFNYCGEFDNAGAMMSIDESLMCSF 305
                                          LORHRLSYVIRSHECKPNGHEFWHDNKIITIFSASNYYAIGSNKGAYIRLNNOLMPHF 405
                                                                                                                                     RGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMGCVPNTLRGAGVWFGPDVTDNF 347
                                                                                                                                                                                                                               YGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGFS-DSTSLDLIKSID
                                                                                                                                                                                                                                                                            LFEYGGFPPEAN-YLFLGDYVDRGKQSLETICLLLAYKIKYPENFFLLRGNHESASINRI 146
                                                                                                                                                                                                                                                                                                                                                                    SGKQVH-----LSEG--EIRQLCAVSKEIFLQQPNLLELEAPIKICGDIHGQYSDLLR
                                                                                                                                                                                  YGFYDECKRRF----NVRLWKIFTDCFNCLPVAALIDDRILCMHGGISPELKSLDQIRNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.6%;
                                                                                            PMDIPESGLVCDLLWSDPSGDVGWGMND-RGVSYTFGADKVAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 434; DB 8;
Pred. No. 8.7e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                      87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                36
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RESULT 32 ADY09284

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90 DIVNAKIELPIRKNHIDLLIDVFRKKRGN--RLHPKYVALILREAAKSLKQLPNISPVST 147

Query Match Best Local S Matches 102

Similarity

12.5%;

Score 431.5; DB Pred. No. 2e-31;

102;

Conservative

66;

Mismatches

125; 8

Indels Length

41;

Gaps

8

Sequence 380

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content. Thi polypeptide invention.
                                            plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert polypeptide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LIUJ/)
(ZHOU/)
(KOVA/)
(SCRE/)
(TABA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAY-1999;
05-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2004034888-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    galactomannan production; lignin production; plant growth regulator;
yield; plant growth; plant development; seed oil; protein yield;
                                                                                                                                                                                                                                                                    ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as
                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 65099; 15pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-APR-2003; 2003US-00425114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant full length insert polypeptide seqid 65099
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                                                                                                                                                                                                                                                                                                   polynucleotide consisting of a sequence encoding an amino acid
available in electronic form from the US patent office at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-180133/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZHOU Y.

ZHOU Y.

KOVALIC D K.

SCREEN S E.

TABASKA J E.
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O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhou Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-00304517.
2001US-00985678.
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                                                                                                                                                                                                                                                                                                                                            describes a recombinant DNA construct comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kovalic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DK,
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ID SP840
ID SP840
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Arabidopsis, wheat and rape but the specification does not indicate whi sequences is derived from which organism. Also included is a method of producing a plant having an improved property, comprising transforming plant with a recombinant DNA construct comprising a promoter region functional in a plant cell operably joined to a polynucleotide encoding polypeptide associated with the property, and growing the transformed plant. The property is selected from improving plant cold tolerance, fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant DNA constructs useful in the field of biochemistry genetics, and in particular for producing transgenic plants with in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-APR-2003;
28-APR-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-DEC-2003; 2003US-00739930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant; transgenic; cold tolerance; growth rate; drought tolerance; disease resistance; galactomannan production; plant growth regulat heat tolerance; herbicide tolerance; lignin production; extreme osmotic condition tolerance; pathogens resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kovalic
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                                                                                                                                                                                                                                                                                                                                                              The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; SEQ ID NO 9917; 14pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-757369/74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant polypeptide,
                                                                                                                                                                                                                                                                                                                         polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biological characteristics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KOVA/) KOVALIC D
                                                                                                                                                                                                                                             invention relates a recombinant DNA construct comprising a nucleotide having any of 5544 nucleotide sequences (CNNAs SEQ ID NO: 44) and encoding a polypeptide with any of 5544 amino acid sequences ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                resistance;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IGSNKGAYIRLMNQLMPHFVQYISAASQTKRLSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LCMHGGLSPDILNLDQIRNLQR------PTDVPDTGLLCDLLWSDPSKEVQ
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2003US-00425115
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                                                                 encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  improved
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RESULT 34
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AC AD708
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DT 21-AF
DT 21-AF
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Plant
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XX
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XW crecom
XW crecom
XW crecom
XW crecom
XW crecom

Plant

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length

insert polypeptide seqid

64475

21-APR-2005 ADY08660; ADY08660

(first

entry)

standard; protein;

plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            not form part of the printed specification, but was obtained electronic format directly from USPTO at segdata.uspto.gov/sequence.html?DocID=20040216190.
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281
                                       388
                                                                                  221
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                                                                                WGESDRGVSCTFGADMLIEFLEKNDLDLICRAHQVVEDGYEFFAQRRLVTIFSAPNYCGE
                                                                                                                                                                                           YPDKVPLLRGNHEDAKINRVYGFYDECKRRF---NVRLWKIFSDCFNCLPIAALIDDKIL
                                                                                                                                                                                                                                                                               FPNAVFLNRGNHEDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVL
                                                                                                                                                                                                                                                                                                                                    IQAPVKICGDIHGQFVDLLKLFDLGGYPPTST-YVFLGDYVDRGKQSLETICLLLAYKIR
                                                                                                                                                                                                                                                                                                                                                                           VSQQVTVCGDLHGKLDDLLVVLHKNGLPSSSNPYVFNGDFVDRGKRGLEVLLLLLSLYLA 208
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FDNVGALLSIDENLMCSF
                                       GSNKGAYIRLNNQLMPHF
                                                                                                                       VPNTLRGAGVWFGPDVTDNFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNYYAI
                                                                                                                                                                   CMHGGLSPELTNLDQIKDIER-----
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298
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Pred. No. 1.9e-31;
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                                                                                                                                                                   -----PABIPDYGLLCDLLWSDPSPDGEG
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                                                                                                                                                                                                                                                                                                                                          The invention describes a recombinant DNA construct comprising a polymucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polymucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, recombination in plants, for improving yield by modification of plant of plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert of homologic invention.
                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          galactomannan production; lignin production; plant growth regulator;
yield; plant growth; plant development; seed oil; protein yield;
                                                                                                                                                                                                                                                                                                    Sequence
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 165
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113; Conserv
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KOVALIC D K.
SCREEN S E.
TABASKA J E.
CAO Y.
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               BAN-YLFLGDYVDRGKQSLETICLLLAYKIKYPENFFLLRGNHECASINRIYGFYDECKR
                                                                         SSNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNARYGFIREVES
                                                                                                                                            NRLHPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLLVVLHKNGLPS
                                                                                                                                                                                                                                                                                                      334 AA;
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RF---NVRLWKVFTECFNTLPVAALIDDKILCMHGGLSPDLAHLDBIKNLQR--
                                                                                                                                                                                                             PQAAGRKNOYQGSAHVSVLDDKDDLVEBFGDIVNAK--IBLPIRKNHIDLLIDVFRKKRG
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                                                                                                                     ---AIFLSQ-----PNLLELEAPIK----ICGDIHGQYSDLLRLFEYGGFPP
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                                                                                                                                                                                                                                         Score 430.5; DB 8;
Pred. No. 2e-31;
7; Mismatches 134;
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RESULT 35
ADY22333
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The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; galactomannan production; lignin production; plant growth regulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant DNA construct, useful for improving plant tolerance cold, heat, drought, herbicides, extreme osmotic conditions, pathoge pests, for conferring increased resistance to plant disease, or for
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05-NOV-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
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(KOVA/)
(SCRE/)
(TABA/)
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yield; plant growth; plant development; seed oil; protein
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ZHOU Y.

KOVALIC D K.

SCREEN S E.

TABASKA J E.

CAO Y.
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2001US-00985678.
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  25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert polypeptide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                       EP1033405-A2
                                                                                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana protein
                                                                                                                                                                                                                                                                                                                                                                                        AAG30063 standard;
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                                                                                                                                                             06-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ICRAHOVVEDGYEFFADROLVTIFSAPNYCGEFDNAGAMMSVDETLMCSF-QILKPAERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NRLHPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLLVVLHKNGLPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                QIYGAKQNV 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VIRSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRLNNQLMPHFVQYISAASQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EAN-YLFIGDYVDRGKQSIETICILLAYKIKYPENFFLLRGNHECASINRIYGFYDECKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSNPYVENGDEVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMAARYGFIREVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----AIFLSQ-----PNLLELEAPIK----ICGDIHGQYSDLLRLFEYGGFPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PQAAGRKNQYQGSAHVSVLDDKDDLVEEFGDIVNAK--IELPIRKNHIDLLIDVFRKKRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KRLSFKORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPLTDGEPLDKTEWQQIFDIMWSDP-QATMGCVPNTLRGAGVWFGPDVTDNFLQRHRLSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RF---NVRLWKVFTECFNTLPVAALIDDKILCMHGGLSPDLAHLDEIKNLQR-----
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                                                                                                                                                                                                                                             sequence
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                                                                                                                                2000EP-00301439
 99US-0121825P.
99US-0123180P.
99US-0123548P.
99US-0125788P.
99US-0126264P.
99US-01267462P.
99US-0127462P.
99US-0128234P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTDVPDQGLLCDLLWSDPGKDVQGWGMND-RGVSYTFGADKVSBFLQRHDLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QGGGGIDAALL---DDIIRRLLEVRTARPGKQVQLSESEIRQLCTVSR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             424
                                                                                                                                                                                                                                                                                                                                                                                        protein;
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Pred. No. 2e-31;
57; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                   fragment
                                                                                                                                                                                                                                                                                                   SEQ ID NO: 35874.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55;
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Plant; transgenic; cold tolerance; growth rate; drought tolerance; disease resistance; galactomannan production; plant growth regulator; heat tolerance; lignin production; extreme osmotic condition tolerance; pathogens resistance; per pest resistance; yield improvement; seed oil yield; seed protein yiel
                                                      Plant polypeptide,
                                                                         13-JAN-2005
                                                                                            ADT57338;
                                                                                                             ADT57338
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                                                                                                                                                                            379
                                                                                                                                                                                                               319
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                                                                                                                                                                                                                                                                   CLLLAYKIKYPENFFLLRGNHESASINRIYGFYDECKRRF---NVRLMKIFTDCFNCLPV
                                                                                                                                                                                                                                                                                                                                                     DIVNAKIELPIRKNHIDLLIDVFRKKR---GNRLHPKYVALILRBAAKSLKQLPNIS---
                                                                                                            standard;
                                                                                                                                                                                                      SDPQATMGCVPNTLRGAGVWFGPDVTDNFLQRHRLSYVIRSHECKPNGHEFMHDNKIITI
                                                                                                                                                                                                                                AALIDDRILCMHGGISPELKSLDQIRNIAR
                                                                                                                                                                                                                                           GSVLNSRVLIVHGGFS-DSTSLDLIKSIDRGKYVSILRPPLTDGBPLDKTEWQQIFDIMW
                                                                                                                                                                                                                                                                            LLLLSLYLAFPNAVFLNRGNHEDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPL
                                                                                                                                                                                                                                                                                                        FLQQPNLLELEAPIKICGDIHGQYSDLLRLFEYGGFPPEAN-YLFLGDYVDRGKQSLETI
                                                                                                                                                                                                                                                                                                                        ----PVSTAVSQQVTVCGDLHGKLDDLLVVLHKNGLPSSSNPYVFNGDFVDRGKRGLEVL
                                                                                                                                                          FSAPNYCGEFDNAGAMMSIDESLMCSF
                                                                                                                                                                           FSASNYYAIGSNKGAYIRLNNQLMPHF
                                                                                                                                                                                             SDPSGDVGWGMND-RGVSYTFGADKVAEFLEKHDMDLICRAHQVVEDGYEFFAERQLVTV
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nilarity 31.2%;
Conservative 6
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                                                                                                            protein;
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S-0161992P.
S-0161993P.
S-0162142P.
                                                                         entry)
                                                        7415.
                                                                                                                                                                                                                                                                                                                                                                               61;
                                                                                                             325
                                                                                                                                                                                                                                                                                                                                                                               Score 430; DB 3;
Pred. No. 1.9e-31;
1; Mismatches 110
                                                                                                                                                                                                                                                                                                                                            -FRNTRPGSGKQVH-----LSEG--EIRQLCAVSKEI
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                                                                                                                                                          291
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protein yield.
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RESULT 37
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XX Plant
Viridiplantae
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                                                                                                                                                                                                                                                                                                                                                         Arabidopsis, wheat and rape but the specification does not indicate which consequences is derived from which organism. Also included is a method of producing a plant having an improved property, comprising transforming a complaint with a recombinant DNA construct comprising a promoter region complaint with a recombinant DNA construct comprising a promoter region complaint with a recombinant DNA construct comprising a promoter region complaint in a plant cell operably joined to a polymucleotide encoding a complaint of the property is selected from improving plant cold tolerance, for plant in growth rate in plant cells by modification of the cell cycle comparished to plant disease, for galactomannan production, for providing increased comproving plant tolerance, for improving plant tolerance, for improving plant tolerance, for improving plant tolerance to herbicides, for increasing the rate of comproving plant tolerance to extreme osmotic conditions, for improving plant tolerance to pathogens or pests, for lignin production, for improving composition of carbohydrate, nitrogen or phosphorus use and/or uptake and for yield improvement by modification of carbohydrate, nitrogen or phosphorus use and/or uptake conditions of also encode a plant transcription factor. The methods and compositions of consostitions of also encode a plant transcription factor. The methods and compositions of consostitions of also encode a plant transcription factor. The methods and compositions of the consostitions of also encode a plant transcription factor. The methods and compositions of the consostitions                                                                                                                                                                                                                                                                                                                                                                                                                                       also encode a plant transcription factor. The methods and compositions of the present invention are useful in the field of biochemistry and genetics, in particular for producing transgenic plants with improved biological characteristics such as increased yield, improved nitrogen flow, increasing plant tolerance to cold or heat, improving plant tolerance to extreme osmotic and drought conditions, and improving plant tolerance to plant pests or pathogens. They can also be used in physical arrays of molecules, plant breeding markers, computer-based storage and analysis systems. The present sequence of the 5544 plant protein sequences of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                      Sequence 325 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates a recombinant DNA construct comprising a polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO: 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-APR-2003; 2003US-00424599 28-APR-2003; 2003US-00425115
                                                                                                                                                                                                                                                                                                                                                                                                             seqdata.uspto.gov/sequence.html?DocID=20040216190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant DNA constructs useful in the field of biochemistry and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-757369/74
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                                        154 TVCGDLHGKLDDLLVVLHKNGLPSSSNPYVFNGDFVDRGKRGLBVLLLLLSLYLAFPNAV 213
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                                                                                                                  14
                                                                                                                                                                                                                                                                  Similarity
KICGDIHGQFVDLLRLFDLGGYPPTST-YIFLGDYVDRGKQSLETICLLLAYKLKYPDNI
                                                                                                                  AAVDEVVRR-----LVEGGRGGRQVQMSEAEIRQLCVEAKQVLLSQPNL----LRIHAPV
                                                                                                                                                                      AKIELPIRKNHIDLLIDVFRKKRGNRLHPKYVALILREAAKSLKQLPNISPVSTAVSQQV
                                                                                                                                                                                                                                                            12.5%;
                                                                                                                                                                                                                                    67;
                                                                                                                                                                                                                                                               Score 429.5; DB 8;
Pred. No. 2.4e-31;
                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                    118;
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                        Length 325;
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The invention relates a recombinant DNA construct comprising a polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO: 1-544) and encoding a polypeptide with any of 5544 amino acid sequences (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean, arabidopsis, wheat and rape but the specification does not indicate which sequences is derived from which organism. Also included is a method of producing a plant having an improved property, comprising transforming a plant with a recombinant DNA construct comprising a promoter region functional in a plant cell operably joined to a polynucleotide encoding a polypeptide associated with the property, and growing the transformed plant. The property is selected from improving plant cold tolerance, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for improving plant drought tolerance, for production of plant growth regulators, for improving plant tolerance, for improving plant tolerance, for plant disease, for galactomannan production, for production of plant growth regulators, for improving plant tolerance, for improving plant tolerance, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant DNA constructs useful in the field of biochemistry and genetics, and in particular for producing transgenic plants with improbiological characteristics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plant; transgenic; cold tolerance; growth rate; drought tolerance; disease resistance; galactomannan production; plant growth regulator; heat tolerance; herbicide tolerance; lignin production; extreme osmotic condition tolerance; pathogens resistance; pest resistance; yield improvement; seed oil yield; seed protein yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-757369/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-APR-2003; 2003US-00425115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-JAN-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADT59253 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-DEC-2003; 2003US-00739930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KOVA/) KOVALIC D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   286 ALLSIDESLMCSF 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; SEQ ID NO 9330; 14pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSPELTSLDQIKDIER------PTEIPDYGLLCDLLWSDPSHDTEGWGESD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YLLRGNHEDAKINRVYGFYDECKRRF---NVRLWKIFCDCFNCLPMAALIDDKILCMHGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID 9330
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RESULT 39
ADY10803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 12.5
Best Local Similarity 30.5
Matches 102; Conservative
                                                                                                                       plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yeald: characteristic plant growth regulator;
Unidentified
                                                                                                 galactomannan production; lignin production; plant growth regulator,
yield; plant growth; plant development; seed oil; protein yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-APR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADY10803,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADY10803 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 326 AA;
                                                                                                                                                                                                                                                                                                                                                                                      Plant full length insert polypeptide seqid 66618.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148 AVSQQVTVCGDLHGKLDDLLVVLHKNGLPSSSNPYVFNGDFVDRGKRGLEVLLLLLSLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90 DIVNAKIELPIRKNHIDLLIDVFRKKRGN--RLHPKYVALILREAAKSLKQLPNISPVST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIVHGGFS-DSTSLDLIKSIDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KYPENFFLLRGNHECASINRIYGFYDECKRRF---NVRLMKTFTECFNCLPVAALIDEKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFPNAVFLNRGNHEDSVMNARYGFIREVBSKYPRNHKRILAFIDEVYRWLPLGSVLNGRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EFDNAGAMMSVDETLMCSF-QILKPADKKVKLNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIK----ICGDVHGQYSDLLRLFEYGGLPPEAN-YLFLGDYVDRGKQSLETICLLLAYKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IGSNKGAYIRLNNQLMPHFVQYISAASQTKRLSF 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LCMHGGLSPDLLNLDQIRNLQR------PTDVPDTGLLCDLLWSDPSKEVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein, 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
Pred.
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No. 2.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 41; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    326
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                                                                                                                                                                                                                                                                                                                                                                            cc polynucleotide consisting of a sequence encoding an amino acid sequence cavailable in electronic form from the US patent office at ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide cof the invention are also useful in physical arrays of molecules and as climproving plant tolerance to cold, heat, drought, herbicides, extreme combination proving pathogens or pests, for manipulating growth rate in conditions, pathogens or pests, for manipulating growth rate in conditions, pathogens or pests, for producing galactomannan, cc increased resistance to plant disease, for producing galactomannan, cc lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake cor by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert construct of the construct of the
                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                          Sequence 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 66618; 15pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-MAY-1999;
05-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-FEB-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   improving yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAOY/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCRE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KOVA/
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ZHOU Y.

KOVALIC D K.

SCREEN S E.

TABASKA J E.

CAO Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhou Y,
QATMGCVPNTLRGAGVWFGPDVTDNFLQRHRLSYVIRSHBCKPNGHBFMHDNKIITIFSA
                                                                  LNSRVLIVHGGFS-DSTSLDLIKSIDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDP
                                                                                                                                   LSLYLAFPNAVFLNRGNHEDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSV
                                                                                                                                                                    QPNLLELEAPIKICGDVHGQYSDLLRLFEYGGYPPDAN-YLFLGDYVDRGKQSIETICLL
                                                                                                                                                                                                    SPVSTAVSQQVTVCGDLHGKLDDLLVVLHKNGLPS8SNPYVFNGDFVDRGKRGLEVLLLL
                                                                                                                                                                                                                                     AGISLPSRSLPGEAMDEAAVDDLIRRLLEARGGRT-PRNAQVTDAEIRRLCAAAKDVFLS
                                                                                                                                                                                                                                                                      AKIELPIR-----KNHIDLLIDVFRKKRGNRLHPKYVALI---LREAAKSLKQLPNI 142
                                                                                                   LAYKIKYPENFFLLRGNHECASINRIYGFFDECKRRF---NVRIWKIFTECFNCLPVAAL
                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                          8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             describes a recombinant DNA construct comprising e consisting of a sequence encoding an amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9908-00304517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kovalic DK,
                                                                                                                                                                                                                                                                                                                       12.5%;
                                                                                                                                                                                                                                                                                                         60;
                                                                                                                                                                                                                                                                                                      Score 429; DB 8;
Pred. No. 2.9e-31;
0; Mismatches 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Screen SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tabaska JE,
                                                                                                                                                                                                                                                                                                         129;
                                                                                                                                                                                                                                                                                                                                     Length 338;
                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                     The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or the proposition of the cell cycle pathway.
                                                      or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert polypeptide that can be used in the recombinant DNA construct of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for
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05-NOV-2001; 2001US-00985678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     growth rate; cell cycle pathway; disease resistance;
galactomannan production; lignin production; plant growth regulator;
yield; plant growth; plant development; seed oil; protein yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbidde tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance;
                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 62750; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                    improving yield.
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SCREEN S E.
TABASKA J E.
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                                                                                                                                                                                           119
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                                                                                             QATMGCVPNTLRGAGVWFGPDVTDNFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSA
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Pred. No. 2.9e-31;
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Search completed: January 20, 2006, 19:48:57 Job time : 139 secs

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Result
No.
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               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:*

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
          GenCore version 5.1.6 (c) 1993 - 2006 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                               US-09-949-016-7370
US-09-217-779-2
US-09-210-767-43457
US-09-248-796A-18327
US-09-248-796A-18327
US-09-248-796A-18323
US-09-248-796A-18323
US-09-248-796A-18323
US-09-538-092-1093
US-09-487-558B-274
US-09-949-016-7363
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Sequence 7370, Apsequence 2, Appli
Sequence 43457, A
Sequence 18327, A
Sequence 18327, A
Sequence 18327, A
Sequence 1093, Appli
Sequence 1093, Appli
Sequence 873, Appli
Sequence 874, App
Sequence 7363, Appli
Sequence 1095, Ap
Sequence 1095, Ap
Sequence 6266, Ap
Sequence 6404, Ap
Sequence 6404, Ap
Sequence 11, Appli
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Sequence 10218, Ap
Sequence 11179, A
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286 IDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMGCVPNTLRGAGVWFGPDVTD 345

Quer Begg Qy Db Qy Db Db	RESULT 1 US-09-944 ; Sequent ; Sequent ; Patent ; GENERAL ; APPLI ; TITLE ; TITLE ; CURREI ; CURREI ; CURREI ; CURREI ; PRIOR FRIOR	233128222233333333333333333333333333333
Query Match Best Local Similarity 33.7%; Matches 143; Conservative  11 FICKWYRRHOARREMORR  12 SYIKGYYRRAASNMALGK-  5 SYIKGYYRRAASNMALGK-  95 YIKGYYRRAASNMALGK-  138 ECNKIVKQKAFERAIAGD  138 ECNKIVKQKAFERAIAGD  138 LIDVFRKKGGNRLHPKYV  108 LIDVFRKKGGNRLHPKYV  1194 LMQWYKDQKKLHRKCA  1194 LMQWYKDQKAFERAIAGD	1 1 249-016-7370 249-016-7370 24L INFORMATION: 24L INFORMATION: 25 OF INVENTER, J. 26 OF INVENTION: 27 OF INVENTION: 28 REFERENCE: CLOOL3 28 REFERENCE: CLOOL3 28 REFILING DATE: 200 29 REFLICATION NUMB 20 REFLICATION NUMB 20 REFLICATION NUMB 21 APPLICATION NUMB 22 REFLING DATE: 200 23 PILING DATE: 200 24 APPLICATION NUMB 25 PILING DATE: 200 26 PILING DATE: 200 27 APPLICATION NUMB 28 PETING DATE: 200 29 REFLICATION NUMB 20 PILING DATE: 200 20 REFLICATION NUMB 21 APPLICATION NUMB 22 PETING DATE: 200 26 PILING DATE: 200 27 APPLICATION NUMB 28 PETING DATE: 200 29 PILING DATE: 200 20 P	391 11.4 319 391 11.4 311 384 11.2 341 11.3 383.5 11.1 312 380 11.0 487 380 11.0 487 380 11.0 487 380 11.0 487 380 11.0 487 380 11.0 530 380 11.0 530 380 11.0 530 370 11.0 535 375 10.9 369 375 10.9 369 376 360 360
Score 570; Pred: No. 2 71; Mismatch CNWQIFQNLEYASFRAA AHV-SVLDKD	US/09949016  g et al. g et al. IN KNOWN GENES RPHISMS IN KNOWN GENES HUMAN DISEASE, METHODS : US/09/949,016 -04-14 60/241,755 -20 60/237,768 -20 60/237,768 60/231,498 -03 50/231,498 -08 Version 4.0	2 US-09-949-016-6461 1 2 US-09-949-016-11335 2 US-09-949-016-8780 2 US-09-949-016-9733 1 US-08-452-722-7 1 US-08-404-731A-7 1 US-08-344-227-7 1 US-08-344-227-7 1 US-08-721-458B-7 2 US-08-721-458B-7 2 US-09-744-016A-9 2 US-09-949-016-1168-3 2 US-09-949-016-1168-2 US-09-487-558B-270 0 US-09-487-558B-268 2 US-09-487-558B-268 2 US-09-82B-796A-18344 9 2 US-09-82B-796A-18344 9 2 US-09-82B-302-13
DB 2; Length 499; 176-46; 176-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-46; 276-	ASSOCIATED OF DETECTION AND USES THEREOF	Sequence 6461, Ap Sequence 11335, A Sequence 11314, A Sequence 11414, A Sequence 7, Appli Sequence 11633, A Sequence 24, Appl Sequence 854, App Sequence 270, App

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RESULT 3
US-09-270-767-43457
; Sequence 43457, Application
; Patent No. 6703491
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US-09-517-779-2
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; SOFTWARE: Patentin Ver.
; SEQ ID NO 2
; LENGTH: 494
; TYPE: PRT
; ORGANISM: Homo sapiens
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APPLICANT: Luo, Ying
APPLICANT: Xu, Xiang
APPLICANT: Xu, Xiang
TITLE OF INVENTION: Cell Cycle Proteins Associated with Rad9, Compositions
TITLE OF INVENTION: and Methods Of Use
FILE REFERENCE: A68293/RMS/DAV
CURRENT APPLICATION NUMBER: US/09/517,779
CURRENT FILING DATE: 2000-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application Patent No. 6660511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                              407
                                                                                                                                                                                                                               363
                                                                                                                                                                                                                                                                                          306 QIYGFEGEVKAKYT---AQMYELFSEVFEWLFLAQCINGKVLIMHGGLFSEDGVTLDDIR 362
                                                                                                                                                                                                                                                                                                                                                         246 NIFELNGLPSETNPYFIFNGDFVDRGSFSVEVILTLFGFKLLYPDHFHLLRGNHETDNMN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   346 NFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRL-NNQLMPH 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 ECNKIVKQKAFERAIAGDEHKRSVVDSLDIESMTIEDEYSGPKLEDGKVTISFMKB----
                                                                                                                              404 HFVQY 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 FIQKWYRRHQARREMQRRCNWQIFQNLEYASEQDQAELYKFFNDLIKHMPQAAGRKNQYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90 YIKGYYRRAASNMALGK-----FR----AALRD-----YETVVKVKPHDKDAKMKYQ 132
                                                                                                                                                                                           DNFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRL-NNQLMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIDVFRKKRGNRLHPKYVALILRBAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FVQY 408
                                                                                                                                                                                                                          KIERNR-----QPP--DSGPM------CDLLWSDPQPQNG-RSISKRGVSCQFGPDVT
                                                                                                                                                                                                                                                        SIDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATWGCVPNTLRGAGVWFGPDVT 344
                                                                                                                                                                                                                                                                                                              ARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVINSRVLIVHCGF--SDSTSLDLIK 284
                                                                                                OFHOF
                                                                                                                                                              KAFLEENNLDYIIRSHEVKAEGYEVAHGGRCVTVFSAPNYCDQMGNKASYIHLQGSDLRP
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                US/09270767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71; Mismatches 142;
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                                               FEATURE:
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; OTHER INFORMATION: Xaa means any amino US-09-270-767-43457
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 43457
LENGTH: 494
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
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Best Local Similarity
Matches 130; Conserv
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                                                                                        384
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428
                                          328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 MPQAAGRKNQYQGSAHVSVLDDKDDLVEEFGDIVNAKIELPIRKNHIDLLIDVFRKKRGN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 NAIRA-AIFIQKWYRRHQARREM----QRRCNWQIFQNLEYASEQDQAELYKFFNDLIKH 58
                            VPNTLRGAGVWFGPDVTDNFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNY 384
                                                                                                                                                                                                            PNAVFINRGNHEDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWIPIGSVLNSRVLI 269
                                                                                                                                                                                                                                                                                                MHGGLPSTEDVTLDHIRRIERN-----CQPP-----EBGLMCELLWSDPQQWMG- 427
                                                                                                                                VHGGF---SDSTSLDLIKSIDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMGC 327
                                                                                                                                                                                                                                                                          EEKFTICGDIHGQFYDLMNIFEINGLPSEKNPYLFNGDFVDRGSFSVECIFTLFGFKLLY
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LGQSKRGVGIQPGPDVTEKFCKDNNLDYIIRSHEVKDMGYEVAHNGKCITVFSASNY
                                                                                                                                                                                  PNHFFLARGNHESINMNOMYGFTGEVTAKYT---SAMADIFTOVFNWLFLCHCINOKILV 383
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Pred. No. 1.4e-41;
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RESULT 4

US-09-248-796A-18327
; Sequence 18327, Application US/09248796A
; Patent No. 6747137
; Patent No. 6747130
; PAPPLICANT: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
; PILLE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US 60/074,725
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR FILING DATE: 1998-08-13
; NUMBER: OF SEQ ID NOS: 28208
; SEQ ID NO 18327
; LENGTH: 445
; TYPE: PRT
ORGANISM: Candida albicans
; PEATURE:
 NAME/KEY: UNSURE
; CCATION: (220), (239)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno

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RESULT 5
US-09-538-092-256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CUTAPATSeqFormatter Version 0.9
SEQ ID NO 256
LENGTH: 312
                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 100; Conserv
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Patent No. 6753314
GENERAL INFORMATION:
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        372
                                                                                                  160 HGKLDDLLVVLHKNGLPSSSNPYVENGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGN
                                                                                                                                                                                            103 NHIDLLIDVFRKKRGNR--LHPKYVALILREAAK-SLKQLPNISPVSTAVSQQVTVCGDL 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194 RGLEVILLILSLYLAFPNAVFLNRGNHEDSVMNARYGFIREVESKYPRNHKRILAFIDEV 253
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      124
                                  220 HEDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGFS-DST 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 416 NGRLMTVFSAPNY 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YRWLPLGSVLNSRVLIVHGGF--SDSTSLDLIKSIDRGKYVSILRPPLTDGEPLDKTEWQ 311
  HECASINRIYGFYDECKRRY--NIKLWKTFTD-CFNCLPIAAIIDEKIFCMHGGLSPDLN 180
                                                                                                                                                         NIIDRLLEVRGSKPGQQVDLEENEIRYLCSKARSIFIKQ----PILLELEAPIKICGDI
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                                                                                HGQYYDLLRLFEYGGFPPESN-YLFLGDYVDRGKQSLETICLLLAYKIKYPENFFILRGN
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                                                                                                                                                                                                                                     12.2%;
ilarity 31.5%;
Conservative 63
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                                                                                                                                                                                                                                     ; Score 418.5; DB 2; Length 312; pred. No. 6.6e-32; 63; Mismatches 125; Indels 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Method of Using
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RESULT 7
US-09-538-092-1093
; Sequence 1093, Application US/09538092
; Patent No. 6753314
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<b>Db</b> .	δ	рь	δ	B &	Db .	<b>2</b> B	. Q	d dy	Query Match Best Local Matches 9	RESULT 6 US-09-248-796 Sequence 18 Patent No. GENERAL INF APPLICANT: TITLE OF II FILE REFER CURRENT FII PRIOR FILII PRIOR PRIOR PRIOR PRILII PRIOR PRIOR PRIOR PRILII PRICIP NO	Q	Db Qy	ος Ας
293 KKPR 296	414 QTKR 417	GYEFFSKRQLVTLFSAPNYCGEFDNAGAMM	354 SYVIRSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRLNNQLMPHFVQYISAAS 413	294 ILREPLIDGEPLOKIEMQQIFOIMMSDPQAIMGCVPNTLKGAGVWFGPDVTDNFLQRHRL 353	CKRRFNIKLMKTFTD-CFNCLPIAAIIDEKIFTMHGGLSPDLNSMEQIRRVMR	73 FPPEAN-YLFLGDYVDRGKQSLETICLLLAYKIKYPENFFILRGNHECASINRIYGFYDB 131 235 VESKYDDNHKDTLAFIDEVYDWLDLGGULNGBULTUHGGES-DGTGLDLIKSIDDGKYVG 203	LPSSSNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNARYGFIRE	118 NRLHPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLLVVLHKNG 174	itch 12.0%; Score 412; DB 2; Length 319; sal Similarity 31.2%; Pred. No. 2.9e-31; 95; Conservative 60; Mismatches 125; Indels 24; Gaps 7;	SULT 6 -09-248-796A-18323 -09-248-796A-18323 Sequence 18323, Application US/09248796A PATENT NO. 6747137 GENERAL INFORMATION: APPLICANT: Keith Weinstock et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.132 CURRENT PPLICATION NUMBER: US/09/248,796A CURRENT FILING DATE: 1999-02-12 PRIOR APPLICATION NUMBER: US 60/074,725 PRIOR PILING DATE: 1999-02-13 PRIOR PILING DATE: 1999-02-13 PRIOR FILING DATE: 1999-08-13 NUMBER OF SEQ ID NOS: 28208 SEQ ID NO 18323 LENGTH: 319 TYPE: PRT ORGANISM: Candida albicans PEATURE: NAME/KEY: UNSURE LOCATION: (16) OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknowned.	399 NQLMPHFVQYISAASQT 415	339 FGPDVTDNFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRLN 398	279 SLDLIKSIDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATWGCVPNTLRGAGVW 338

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; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PATENTIN VET. 2.0
; SEQ ID NO 6
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-167-206-6
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CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/17,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CURAPAtSeqFormatter Version 0.9
SEQ ID NO 1093
LENGTH: 323
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US-09-167-206-6
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                                                                                                                                                                                                                                                                    Sequence 6, Application US/09167206A Patent No. 6476193
GENERAL INFORMATION:
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APPLICANT: Glot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 105; Conserv
 Query Match
                                                                                                                                           APPLICANT: Nandabalan, Krishnan
APPLICANT: Schulz, Vincent P.
APPLICANT: Yang, Meija
TITLE OF INVENTION: NIK1 PROTEIN AND NIK1 PROTEIN COMPLEXES
FILE REFERENCE: 15966-521 NIK1 protein complexes
CURRENT APPLICATION NUMBER: US/09/167,206A
CURRENT FILING DATE: 1998-10-06
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LOCATION: (0)...(0)
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 11.7%;
 Score 403.5;
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APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER: 09/178,965
PRIOR FILING DATE: 2000-03-01
NUMBER: 09/178,965
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LENGTH: 330
TYPE: PRT
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NAME/KEY: misc_feature
LOCATION: (0)...(0)
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                                                                                                                                                                                                                                                                                                                                                                                        102 KNHIDLLIDVFRKKRGNRLHPKYVALI---LREAAKSLKQLPNISPVSTAVSQQVTVCGD
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TSLDLIKSIDRGKYVSILRPPLTDGBPLDKTEWQQIFDIMWSDPQATMGCVPNTLRGAGV 337
                                                                                        NHECASINRIYGFYDECKRRY--NIKLWKTFTD-CFNCLPIAAIVDEKIFCCHGGLSPDL 180
                                                                                                                                               NHEDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGF8-DS
                                                                                                                                                                                                          IHGQYYDLLRLFEYGGFPPESN-YLFLGDYVDRGKQSLETICLLLAYKIKYPENFFLLRG
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CURRENT APPLICATION NUMBER: US/09/744,016A
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: EB98113876
PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 33
LENGTH: 524
TYPE: PRT
ORGANISM: Homo sapiens
US-09-744-016A-33
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US-09-744-016A-33
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PATENT NO. 6875581
GENERAL INFORMATION:
APPLICANT: Dr. Voelkel, Helge
TITLE OF INVENTION: Method for screening of modulators of calcineurin
TITLE OF INVENTION: Activity
FILE REFERENCE: A34157FCT
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Best Local :
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435 TGTLPLGVLSGGKQTIB--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 NAKIBLPIRKNHIDLLIDVFRKKRGNRLHPKYVALILREAAKSLKQLPNISPVSTAVSQQ 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46 NGKPKVDVLKNHL-----VKEG-RLEEEVALKIINDGAAILRQ----EKTMIEVDAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                      EHYTHNTVRGCSYFYSYPAVCEFLONNNLLSIIRAHEAQDAGYRMYRKSQATGFPSLITI
                                                                                                                                                                                                                                                                                                                                                                                                                     GPS-DSTSLDLIKSIDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMG-----
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                                   AIDLLVAHMPGAYSKAEMLEKCRMMDLNGDGKVDLNEFLEAFRLSDLHRKEQQDENIR 611
                                                                                                             NRTLDLLDTDVILEAEADG-MSVMDALYANK----ASLVAIFNIIDADNSGEITLDEFET 553
                                                                                                                                                                                      MRDHRDELEDEFRKYDPKDSGYISISHWCKVMENVTKLGLPWRLLRDKLAPGTDSQKVNY 498
                                                                                                                                                                                                                              FSAPNYLDVYNNKAAVLKYENNVM-----
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                                                                         NVLNICSDDELISDDEAEGSTTVRKEIIRNKIRAIGKMARVFSILRQESESVLTLKGLTP 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.7%; Score 403; DB 2; Length 524; llarity 25.3%; Pred. No. 5.1e-30; Conservative 78; Mismatches 202; Indels 1
                                                                                                                                                   --NIROFNCSPHPY-----WLPNFMDVFTWSLPF-----VGEKVTEMLV
-----TAKQEAAEEREAIRGFSLQHKIRSFEEAR 480
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CURRENT FILING DATE: 2000-01-19;
PRIOR APPLICATION NUMBER: US 60/487,558;
PRIOR FILING DATE: 1999-10-20;
NUMBER OF SEQ ID NOS: 446;
SOFTWARE: PatentIn version 3.0;
SEQ ID NO 274;
LENGTH: 692;
TYPE: PRT
CORGANISM: Saccharomyces cerevisiae
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US-09-487-558B-274
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Patent No. 694935
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TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.130
CURRENT APPLICATION NUMBER: US/09/487,558B
CURRENT FILING DATE: 2000-01-19
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 351 KNAPKKFKKPIDIDETIQKLLDAGYAAKRTKNVCLKNNEILQICIKARBIFLSQPSLLEL
670 R 670
                                                                    626 NYCGBFDNWGAVMSVSEGLLCSF--
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                                                                                                                                                                                                                                     LNSRVLIVHGGFSDSTSLDLIKSIDRGKYVSILRPPLTDGBPLDKTBWQQIFDIMWSDPQ
                                                                                                                                                                                                                                                                                                                 LSLYLAFPNAVFLNRGNHEDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSV
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                                                                                                    NYYAIGSNKGAYIRLNNQLMPHFVQYISAASQTKRLSFKQRMGIVESSALKELAVRMRDH 442
                                                                                                                                                                                                              VAGKIFCVHGGLS-----PVLNSMDEIRHVV-----RPTDVPDFGLINDLLWSDPT
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Milne, Todd
No. 6949356man,
Royer, John
Salama, Sofie
Sherman, Amir
Silva, Jeff
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Madden, Kevin
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28.5%; Pred. No. 8.1e-30;
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                                                                   ELLDPLDSAALKQVMKKGRQE
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RESULT 12 US-09-949-016-7363 ; Sequence 7363, Application US/09949016 ; Patent No. 6812339

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; NAME/KEY: misc_feature
; LICCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P37140
US-09-538-092-1095
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; Sequence 1095, Application US/09538092
; Patent No. 6753314
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                              NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version SEQ ID NO 1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 207012
SOPTWARE: FastSEQ for Windows Version
SEQ ID NO 7363
LENGTH: 374
TYPE: PRI
ORGANISM: Human
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/538,092 CURRENT FILING DATE: 2000-03-29 PRIOR APPLICATION NUMBER: 60/127,352 PRIOR FILING DATE: 1999-04-01 PRIOR APPLICATION NUMBER: 60/178,965 PRIOR FILING DATE: 2000-02-01
                                                                                                                                                                                                                                                                                                                              APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes
FILE REFERENCE: 15966-542
                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                             FEATURE:
                                                                                                                                      ENGTH: 327
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US-09-949-016-6266
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PASESEQ for Windows Version
SEQ ID NO 6266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6266, Application US/09949016 Patent No. 6812339 GENERAL INFORMATION:
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Best Local :
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307

FULL REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/99/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768
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  SMEQIRRIMR --
                                                                             HECASINRIYGFYDECKRRF--NIKLWKTFTD-CFNCLPIAAIVDEKIFCCHGGLSPDLQ 180
                                                                                                                   HEDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGF8-DST 278
                                                                                                                                                           HGQYTDLLRLFEYGGFPPEAN-YLFLGDYVDRGKQSLETICLLLAYKIKYPENFFLLRGN
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                                   SLDLIKSIDRGKYVSILRPPLTDGSPLDKTSWQQIFDIMWSDPQATMGCVPNTLRGAGVW 338
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31.3%; Pred. No. 2.9e-30;
tive 57; Mismatches 128
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; Pred. No. 2.9e-30;
57; Mismatches 128
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-90-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PastSEQ for Windows Version 4.0

LENGTH: 356
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US-09-949-016-6642
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US-09-949-016-8084
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               GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHIANS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISBASE, METHODS OF DETECTION AND
                                                                                      Sequence 6642, Application US/09949016 Patent No. 6812339
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Best Local Similarity
Matches 96; Conserv
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-09-949-016-8084
FILE REFERENCE: CL001307
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; Pred. No. 3.3e-30;
57; Mismatches 128;
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; Sequence 12, Application US/09744016A
; Patent NO. 6875581
; GENERAL INFORMATION:
; APPLICANT: Dr. Voelkel, Helge
; TITLE OF INVENTION: Method for screening of modulators of calcineurin
TITLE OF INVENTION: activity
; FILE REFERENCE: A34157PCT
; CURRENT APPLICATION NUMBER: US/09/744,016A
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: EP98113876
; PRIOR FILING DATE: 1998-07-22
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 12
LENGTH: 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6642
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US-09-744-016A-12
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 502
                                                                            Query Match 11.7%;
Best Local Similarity 31.7%;
Matches 106; Conservative 5.
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ORGANISM: Homo sapiens
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                                     93 NAKIELPIRKNHIDLLIDVFRKKRGNRLHPKYVALILREAAKSLKQLPNISPVSTAVSQQ 152
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NGKPKVDVLKNHL---
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31.7%;
----VKEG-RLEBEVALKIINDGAAILRQ----BKTMIBVDAP
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                                                                            Score 402; DB 2
Pred. No. 6e-30;
4; Mismatches 1
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Pred. No. 5.9e-30;
4; Mismatches 120
                                                                                                                 DB 2;
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GENERAL INFORMATION:
APPLICANT: Dr. Voelkel, Helge
ITITLE OF INVENTION: method for screening of mod
ITITLE OF INVENTION: activity
FILE REFERENCE: A34157PCT
CURRENT APPLICATION NUMBER: US/09/744,016A
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: EP98113876
PRIOR APPLICATION NUMBER: EP98113876
PRIOR PILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
LENGTH: 514
TYPE: PRT
ROBANISM: Homo sapiens
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Best Local S
Matches 106
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Local Similarity 31.7%; Pred. No. 6.1e-30;
nes 106; Conservative 54; Mismatches 120; Indels
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                                                                                                                             ---CVPNTLRGAGVWFGPDVTDNFLQRHRLSYVIRSHECKPNGHEFMHDNK-----IITI
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                                                                             FSASNYYAIGSNKGAYIRLNNQLM-----PH 404
                                                                                                        EHYTHNTVRGCSYFYSYPAVCEFLQNNNLLSIIRAHBAQDAGYRMYRKSQATGFPSLITI
                                                                                                                                                                     GMSPEITSLDDIRKLDR----FTEPP-----AFGPVCDLLWSDPSEDYGNEKTL
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                                               FSAPNYLDVYNNKAAVLKYENNVMNIRQFNCSPH 347
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US-09-190-976B-8
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
COMPUTER: Dell PC
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                                                          STATE: Massachusetts
COUNTRY: USA
                                               ZIP: 01930
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RESULT 19

3.50 inch,

1.40

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storage

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; LENGTH: 535
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11179
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastESEQ for Windows Version 4.0

SEQ ID NO 11179
                                                                                                                                                                                                                                                                                       Sequence 8, Application US/09190976B Patent No. 6815187 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 106; Conserv
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSES: David Prashker,
STREET: P.O. Box 5387
CITY: Magnolia
                                                                                                                                                              TITLE OF INVENTION: Stimulation of angiogenesis via syndecan-4 cytoplasmic domain signaling pathway
                                                                                                                                                                                                                                                                APPLICANT: Simons, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 ITVCGDIHGQFFDLMKLFEVGGSPSNTR-YLFLGDYVDRGYFSIBCVLYLWSLKINHPKT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213 VFLNRGNHEDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FSAPNYLDVYNNKAAVLKYENNVMNIRQFNCSPH
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                                                                                                                                                                                                                            Horowitz, Arie
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FILING DATE: 12-No. 6815187-1998
CLASSIFICATION: Unknown
ATTORNEY/AGENT INFORMATION:
NAME: David Prashker, Esq.
REGISTRATION NUMBER: 29,693
REFERENCE/DOCKET NUMBER: BIS-041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (978) 525-3794
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                        Sequence 276, Application US/09487558B Patent No. 6949356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 100;
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           APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Sulva, Jeff
APPLICANT: Sunmars, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite
FILE REFERENCE: 109272.130
CURRENT APPLICATION NUMBER: US/09/487,558B
                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                  APPLICANT: Busby, APPLICANT: Cali,
                                                                                                                                                   APPLICANT:
                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 KNHIDLLIDVFRKKRGNRLHPKYVALI----LREAAKSLKQLPNISPVSTAVSQQVTVCGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 LHGKLDDLLVVLHKNGLPSSSNPYVFNGDFYDRGKRGLEVLLLLLSLYLAFPNAVFLNRG
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                                                                                                                                                               Maxon, Mary
Milne, Todd
No. 6949356man,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DETLMCSF-QILKPADKNK 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSLDLIKSIDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMGCVPNTLRGAGV 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NHECASINRIYGFYDECKRRY--NIKLWKTFTD-CFNCLPIAAIVDEKIFCCHGGLSPDL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IHGQYYDLLRLFBYGGFPPBSN-YLFLGDYVDRBKQSLBTICLLLAYKIKYPENFFLLRG
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Holtzman, Doug
Madden, Kevin
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                                                                                                                                                 Royer, John
                                                                                                                                                                                                                                                                                    Cali, Brian
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2000-01-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.5%; Score 395.5; DB 2; Length 31.3%; Pred. No. 1.3e-29; tive 60; Mismatches 134; Indels
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102 KNHIDLLIDVFRKKRGNRLHPKYVALILRBAAKSLKQLPNISPVSTAVSQQVTVCGDLHG 161

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FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-37,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER: OF SEQ ID NOS: 207012

SOPTWARE: FBSESEQ for Windows Version 4.0

SEQ ID NO 10218

LENGTH: 502
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; Sequence 10218, Application US/09949016
; Patent No. 6812339
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                                                                                              ; ORGANISM: Human US-09-949-016-10218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/487,558
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 446
SOPTWARE: PatentIn version 3.0
SEQ ID NO 276
LENGTH: 710
TYPE: PRT
Query Match
Best Local Similarity
Matches 101; Conserv
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                                                                                                                                           TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              281 DLIKSIDRGKYVSILRÞÞLTDGEÞLDKTEWQQIFDIMWSDÞQATMGCVÞNTLRGAGVWFG 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            339 PRGKGQRSSSSSSSSSQRIYVSPPSPTGDFVHGSCADGDNGSRTNTMVEMKRKKPVRPVDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 PQAAGRKNQYQGSA----HVSVLDDKDDLVB-----EFGDIVNAKIEL----PIRKNHI
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  Conservative
11.4%; Score 391.5; DB 2; 31.1%; Pred. No. 6.2e-29; tive 58; Mismatches 119;
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RESULT 23
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SCOTTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 510
TYPE: PRT
ORGANISM: Homo sapiens
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PATENT NO. 6875581
GENERAL INFORMATION:
APPLICANT: Dr. Voelkel, Helge
TITLE OF INVENTION: Method for screening of modulators of calcineurin
TITLE OF INVENTION: activity
FILE REFERENCE: A34157PCT
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: EP98113876
PRIOR APPLICATION NUMBER: EP98113876
PRIOR FILING DATE: 1998-07-22
NUMBER OF SECT IN NOC. 22
NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN NUMBER OF SECT IN SECT
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YNNKAAVLKYENNVMNIRQFNCSPH
                                                                                                                                  GCSYFYSYPAVCEFLOHNNLLSILRAHEAQDAGYRMYRKSQTTGFPSLITIFSAPNYLDV
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31.1%; Pred. No. 6.4e-29;
ative 58; Mismatches 119;
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US-09-538-092-1283
RESULT 25
US-09-744-016A-21
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SOFTWARE: CuraPatSeqFormatter Version
SEQ ID NO 1283
LENGTH: 521
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Best Local Similarity
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APPLICANT: Mansfield, Traci A.
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
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PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
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PRATURE:
NAMS/KBY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number Q08209
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Pred. No. 6.6e-29
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Sequence 21, Application US/09744016A

Patent No. 6875581

Patent No. 6875581

GENERAL IMPORMATION:
APPLICANT: Dr. Voelkel, Helge
ITILE OF INVENTION: Method for screening of modulators of calcineurin
TITLE OF INVENTION: activity
PILE REFERENCE: A34157PCT
CURRENT APPLICATION NUMBER: US/09/744,016A

CURRENT ETLING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: EP98113876
PRIOR APPLICATION NUMBER: EP98113876
PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21

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; LENGTH: 533
; TYPE: PRT
; ORGANISM: Homo B
US-09-744-016A-18
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US-09-744-016A-18
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/744,016A
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: EP98113876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dr. Voelkel, Helge
TITLE OF INVENTION: Method for screening of modulators of calcineurin
TITLE OF INVENTION: activity
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ORGANISM: Homo
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                281 DLIKSIDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMG-----CVPNTLR
                                                                                                                                                                                                                              102 KNHIDLLIDVFRKKRGNRLHPKYVALILRBAAKSLKQLPNISPVSTAVSQQVTVCGDLHG
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                                                                                                                                                                                                                                                                 101;
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                                                    CRHLTEYFTFKQECKIKY---SERVYDACMDAFDCLFLAALMNQQFLCVHGGLSPEINTL
                                                                                                                          QFFDLMKLFEVGGSPANTR-YLFLGDYVDRGYFSIECVLYLWALKILYPKTLFLLRGNHB
                                                                                                                                                                                             KPRVDILKAHLMKE--GRLEESVALRIITEGASILRQEKNLLDIDA----PVTVCGDIHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YNNKAAVLKYENNVMNIRQFNCSPH 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDIRKLDRFK-----EPP-----AYGPMCDILWSDPLEDFGNEKTQEHFTHNTVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QFFDLMKLFEVGGSPANTR-YLFLGDYVDRGYFSIECVLYLWALKILYPKTLFLLRGNHE
                                                                                       DSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGFS-DSTSL
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                                                                                                                                                                                                                                                               11.4%; Score 391.5; DB 2; 31.1%; Pred. No. 6.9e-29; ative 58; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 391.5; DB 2
Pred. No. 6.6e-29;
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US-09-949-016-6461
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US-09-538-092-902
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                  GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes
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Patent No. 67533
                                                                                                                                 Sequence 6461, Application US/09949016 Patent No. 6812339
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CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
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SOFTWARE: CuraPatSeqFormatter Version
CURRENT APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P11082
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                                                                                                                                                                                                                                                                                                           356 VIRSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRLNNQLMPHFVQY 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 RLHPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLLVVLHKNGLPSS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 YPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGFSDS-TSLDLIKSIDRGKYVSILRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 TN-YLFMGDYVDRGYYSVETVTLLVALKVRYPERITILRGNHESRQITQVYGFYDBCLRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 QLNENQVRTLCEKAKEILTKESNVQEVRC----PVTVCGDVHGQFHDLMELFRIGGKSPD
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                                                                                                                                                                                                                                                                                                                                                                                                          PLTDGEPLDKTEWQQIFDIMWSDP--QATMGCVPNTLRGAGVWFGPDVTDNFLQRHRLSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y--GNANVWKYFTDLFDYLPLTALVDGQIFCLHGGLSPSIDTLDHIRALDRLQEVPHEGP
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NUMBER: US/09/949,016
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION UNMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FRANCE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6461
PRIOR DESCRIPTION OF TYPE: PRI
PRIOR HUMAN
US-09-949-016-6461
                                                                                                                                                                                                      FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: U8/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-3

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTEEQ for Windows Version 4.0

SEQ ID NO 11335

LENGTH: 311

TYPE: PRT

ORGANISM: Human
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US-09-949-016-11335
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Best Local S
Matches 92
                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6812339
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                                                                                                                                                                                          -09-949-016-11335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                    119 RLHPKYVALILRBAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLLVVLHKNGLPSS 178
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                                                                                                                   Similarity
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QLNENQVRTLCEKAKEILTKESNVQEVRC----PVTVCGDVHGQFHDLMELFRIGGKSPD
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                                                                                                                11.4%; Score 391; DB 2; 31.4%; Pred. No. 3.1e-29;
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                                                                                        Mismatches 110;
                                                                                                                                    Length 311;
                                                                                          Indels
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GENERAL INFORMATION:

APPLICANY: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

PILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOPTWARE: PASESEQ for Windows Version 4.0
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US-09-949-016-8780
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Best Local Similarity
Matches 98; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8780, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Human
  317
                                                                                                                                               345 DNFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRLNNQLMPH 404
                                                                                                                                                                                                                                                                                               155
                                                                                                                                                                                                                                                                                                                                                                                                                        166 LLVVLHKNGLESSSNEYVENGDEVDRGKRGLEVLLLLLSLYLAFENAVFLNRGNHEDSVM 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        356 VIRSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRLNNQLMPHFVQY 408
                                                                                                                                                                                                                                            285 SIDRGKYVSILRÞPLIDGEPLDKIEWQQIFDIMWSDPQATMGCVPNTLRGAGVWFGPDVT 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 DLLIDVFRKKRGNRLHPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDD
                                                                                                                                                                                                                                                                                                                                                                                              96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 DLDRQIEQLRRCELIKESEVKALCAKAREILVEESNVQ----RVDSPVTVCGDIHGQFYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNPYVENGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNARYGFIREVESK 238
FIIFEAAPQETRGIPSKK 334
                                                  FVQYISAASQTKRLSFKQ 422
                                                                                                                                                                                                                                                                                               TQVYGFYDECLRKY---GSVTVWRYCTEIFDYLSLSAIIDGKIFCVHGGLSPSIQTLDQIR
                                                                                                                                                                                                                                                                                                                                            NARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGFSDS-TSLDLIK 284
                                                                                                                                                                                                                                                                                                                                                                                              LKELFRVGGDVPETN-YLFMGDFVDRGFYSVETFLLLLALKVRYPDRITLIRGNHESRQI 154
                                                                                               AQFNAANDIDMICRAHQLVMBGYKWHFNBTVLTVWSAPNYCYRCGNVAAILBLDBHLQKD
                                                                                                                                                                                               TIDRKQEVP-----HDG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y--GNANVWKYFTDLFDYLPLTALVDGQIFCLHGGLSPSIDTLDHIRALDRLQEVPHEGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGFSDS-TSLDLIKSIDRGKYVSILRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----MCDLLWSDPDDRGGWGISP---RGAGYTFGQDISETFNHANGLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.2%; Score 386; DB 2; 30.8%; Pred. No. 1.1e-28; tive 63; Mismatches 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24;
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RESULT 31 US-09-949-016-11414

Indels Length 312;

53;

10

163

223

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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOPTWARE: FRASTSEQ for Windows Version 4.0
SEQ ID NO 9733
LENGTH: 312
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US-09-949-016-9733
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US-09-949-016-11414
                                                                                                                                                                                                                                                                                                        Sequence 9733, Application US/09949016
PATENT NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
PILE REFERENCE: CL001307
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SEQ ID NO 11414
LENGTH: 355
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Best Local Similarity
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER: FILING DATE: 2000-09-08
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Patent No. 6812339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIN-YLFMGDYVDRGYYSVETVTLLVALKVRYRERITILRGNHESRQITQVYGFYDECLR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KY--GNANVWKYFTDLFDYLFLTALVDGQIFCLHGGLSPSIDTLDHIRALDRLQEVPHEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGFSDS-TSLDLIKSIDRGKYVSILR 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KQLSESQVKSLCEKAKEILTKESNVQEVRC----PVTVCGDVHGQFHDLMELFRIGGKSP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRSAERQPAGAGGIMDEKVFTKELDQWIEQLNEC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.2%; Score 384; DB 2; Length 355; 27.7%; Pred. No. 1.9e-28;
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US-09-949-016-9733
                                                  ; MOLECULE TYPE: US-08-452-722-7
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  Query Match
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                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,227
FILING DATE: 23-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/G100
                                                                                                                                                                                                    TELEFAX: 312-4740448
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION: APPLICANT: Scott,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM:
                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Calcineurin Inhib: TITLE OF INVENTION: Anchoring Protein
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STREET: 25
STREET: 27
Thinoi
                                                                                                                                                                                                      TELEPHONE: 312-4740448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 30-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                    TOPOLOGY:
                                                                                                                                 TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225 AKVINEFVHINNIKKLICRAHQLVHEGYKFMFDEKLVIVWSAPNYCYRCGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  341 PDVTDNFLORHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNY-YAIGS 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       283 IKSIDRGKYVSILRPPLTDGEPLDKTEWQQIPDIMWSDPQ--ATMGCVPNTLRGAGVWFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 QITQVYĞFYDECQTKY--GNANAWRYCTKVFDMLTVAALIDEQILCVHĞĞLİSPDIKTLDQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224 VMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGFS-DSTSLDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 DDLLVVLHKNGLPSSSNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 YDLCELFRTGGQVPDTN-YIFMGDFVDRGYYSLETFTYLLALKAKWPDRITLLRGNHESR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 KYV-----BIARLCKYLPENDLKRLCDYVCDLLLEBSNVQPVST----PVTVCGDIHGQF 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97;
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                                                                                                                         amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                      amino acids
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                                                                          protein
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  11.0%;
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Score 380;
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Length 487;
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274

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APPLICATION: 435
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/344,227
FILING DATE: 23-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/325
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 312-474-6300
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US-08-404-731A-7
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 30.1
Matches 101; Conservative
Query Match
Best Local Similarity
                                                                                                                                                                           TELEFAX: 312-4740448
INFORMATION FOR SEQ ID NO:
                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,731A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lockerbie, Robert Owen, et al. TITLE OF INVENTION: Calcineurin Inhibitory TITLE OF INVENTION: Anchoring Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Chicago
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11.0%;
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tive 57; Mismatches 115;
                                                                                                                                                                                                                                                        27866/32532
Score 380; DB 1;
Pred. No. 7.7e-28;
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US-08-344-227-7
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                                                                                                                           US-08-344-227-7
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                                                                     Query Match
Best Local Similarity
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                                                      Matches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: SCOTE, John D.
TITLE OF INVENTION: Calci
TITLE OF INVENTION: Ancho
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                           TELEFAX: 312-4740448
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acid
                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
NEGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive, 6300 Sears Tower
332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLDDIRRLDRFK-----EPP-----AFGPMCDLLWSDPSEDFGNEKSQEHFSHNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLDLIKSIDRGKYVSILRPPLIDGEPLDKTEWQQIFDIMWSDPQATMG-----CVPNT 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HÉCRHLTEYFTFKQÉCKIKY---SERVYEACMÉAFDSLPLAALLNQQFLCVHGGLSPEIH 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGFS-DST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Illinois
                                                                                                                                                                                            487 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  United States
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                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                     11.0%; Score 380; DB 1; 30.9%; Pred. No. 7.7e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anchoring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Calcineurin Inhibitory Compounds and
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                                                  57;
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                                                                                                                                                                                                                                                                                                      27866/G1000
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                                                    Mismatches 115; Indels 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                     Length 487;
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US-08-503-226B-7
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                 Matches 101;
                                                        Query Match
                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/404,731
PILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,227
PILING DATE: 23-NOV-1994
PILING DATE: 23-NOV-1994
ATTORNEY/AGENT INPORMATION:
                                                                                                                            INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOPTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/503,226B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Marchall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive, 6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Calcineuri
                                                                                                            TOPOLOGY: 11
                                                                                                                                                                                                                                         TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                 Local Similarity
                                                                                                                                                                                                                                                                              NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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                   Conservative
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                   57;
                                 Score 380; DB 1; Length 487; Pred. No. 7.7e-28;
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                 Mismatches 115;
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Inhibitory
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GENERAL INCOMMATION:
                                                                                                          TELEFAX: 312-4740448
INFORMATION FOR SEQ ID NO:
                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 0 FILING DATE: 23-NOV-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
US 08/344,227
                                                                                                                                                                                                                                                                                                                                                                                     PILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                               REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                    FILING DATE: 17-JUL-1995
ATTORNBY/AGENT INFORMATION:
NAME: Williams Jr., Joseph
REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                 TYPE: ami
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                                                                       LENGTH:
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                                                                       487 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    United States of America
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APPLICANT: Dr. Voelkel, Helge
TITILE OF INVENTION: Method for screening of mod
TITILE OF INVENTION: Activity
FILE REFERENCE: A34157PCT
CURRENT APPLICATION NUMBER: US/09/744,016A
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: BP98113876
PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 528
TYPE: PRT
ORGANISM: Homo sapiens
US-09-744-016A-9
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Best Local Similarity
Matches 101; Conserv
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Best Local Similarity
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 TLDDIRRLDRFK----EPP
                                                                                                           HECRHLTEYFTFKOECKIKY---SERVYEACMEAFDSLPLAALLNOOFLCVHGGLSPEIH 220
                                                                                                                                                                        HGQFFDLMXLFEVGGSPANTR-YLFLGDYVDRGYFSIECVLYLWVLKILYPSTLFLLRGN
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                                                                             SLDLIKSIDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMG-----CVPNT
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                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                 11.0%; Score 380; DB 2; Length 528; 30.9%; Pred. No. 8.9e-28; tive 57; Mismatches 115; Indels
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US-09-744-016A-24
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; ORGANISM: Human
US-09-949-016-11683
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                                                                                                        Sequence 24, Application US/09744016A Patent No. 6875581 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 101;
APPLICANT: Dr. Voelkel, Helge TITLE OF INVENTION: Method for screening of modulators TITLE OF INVENTION: Activity FILE REFERENCE: A34157PCT CURRENT APPLICATION NUMBER: US/09/744,016A CURRENT APPLICATION NUMBER: BP98113876 PRIOR APPLICATION NUMBER: BP98113876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 530
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows
SEQ ID NO 11683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11683, Approximately Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CLOO1307
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DVYNNKAAVLKYENNVMNIRQFNCSPH 354
                                                 AIGSNKGAYIRLNNQLM-----PH 404
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Pred. No. 8.9e-28;
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; PRIOR FILING DATE: 1998-07-22; NUMBER OF SEQ ID NOS: 35; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 24; LENGTH: 535; TYPE: PRT; ORGANISM: Homo sapiens US-09-744-016A-24
Search completed: January 20, 2006, 19:53:38 Job time: 48 secs
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                                                                         333 DYYNNKAAVLKYENNVMNIRQFNCSPH 359
                                                                                                                386 AIGSNKGAYIRLNNQLM-----PH 404
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Maximum Match 100%
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Match Length
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2: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

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5: /cgn2_6/ptodata/1/pubpaa/US11B_PUBCOMB.pep:*
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US-10-369-493-5651
US-10-369-493-5651
US-10-287-226-324
US-10-287-226-326
US-10-425-115-347492
US-10-425-135-3610
US-10-437-963-195520
US-10-437-963-963-9630
US-10-332-923-9610
US-10-298-638-7
US-10-298-638-7
US-10-298-638-7
US-10-298-638-7
US-10-298-638-7
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US-10-298-638-7
US-10-298-638-7
US-10-369-493-22595
US-10-369-493-30347
US-10-369-493-313007
US-10-425-115-225312
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US-10-425-115-225312
US-10-425-115-225312
US-10-425-114-590385
US-10-425-114-590385
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              Sequence 9610, Ap
Sequence 296, App
Sequence 9609, App
Sequence 10, Appl
Sequence 191442,
Sequence 28, Appl
Sequence 28, Appl
Sequence 2595, A
Sequence 4091, App
Sequence 5988, Ap
Sequence 5988, Ap
Sequence 21980, A
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 50385, A
Sequence 50385, A
Sequence 50385, A
Sequence 50385, A
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 41259, A
Sequence 5651, App
Sequence 324, App
Sequence 326, App
Sequence 347492,
Sequence 61206, A
Sequence 18312, A
Sequence 18312, A
Sequence 40348, A
Sequence 19520,
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	0
423	425	426	426	426.5	426.5	427	427	427.5	427.5	428.5	429	429	429.5	429.5	430.5	430.5	1 C C C
12.3	12.3	12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.5	12.5	12.5	12.5	12.5	12.5	14.0
290	401	324	297	325	322	329	322	322	316	428	338	338	326	325	334	334	
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US-10-425-114-38024	US-10-369-493-6597	US-10-425-115-200192	US-10-425-115-195309	US-10-437-963-106229	US-10-425-115-293336	US-10-424-599-194787	US-10-437-963-111414	US-10-425-115-293335	US-10-369-493-2574	US-10-437-963-104697	US-10-425-114-66618	US-10-425-114-62750	US-10-739-930-9330	US-10-739-930-7415	US-10-425-114-70117	US-10-425-114-64475	00-10-739-3317
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	peducine
38024, 7	6597, Ap	200192,	195309,	106229,	293336,	194787,	111414,	293335,	2574, Ap	104697,	66618, 7	.62750, 1	9330, Ag	7415, Ap	70117, 1	64475, I	27111

## ALIGNMENTS

RESULT 1 US-11-097-143-41259

Sequence 41259, Application US/ Publication No. US20050208558A1 GENERAL INFORMATION:

US/11097143

EXPRESSION OF 10,000 OR MORE

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CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT PILING DATE: 2005-04-04
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-19
PRIOR PILING DATE: 1999-10-19
PRIOR PILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR PILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-12-28
PRIOR PILING DATE: 1999-12-28
PRIOR PILING DATE: 1999-12-28
PRIOR PILING DATE: 2000-01-3,383
PRIOR PILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR PILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 2000-03-24
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PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 2010-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: PASESEQ FOR WINDOWS Version 4.0
SEQ ID NO 41259
LENCTH: 637
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Best Local S
Matches 637
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APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS
TITLE OF INVENTION: ARRAYS, FOR DETECTING
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REPERENCE: CL000728
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 637
TYPE: PRT
ORGANISM: DROSOPHILA
145 VSTAVSQQVTVCGDLHGKLDDLLVVLHKNGLPSSSNPYVFNGDFVDRGKRGLEVLLLLLS
                                                                                                                                                                                                                                                                                                            637;
                                                             61 VEEFGDIVNAKIELPIRKNHIDLLIDVFRKKRGNRLHPKYVALILREAAKSLKQLPNISP
                                                                                                                                                                                                                                            25 MORRCNWQIFQNLEYASEQDQAELYKFFNDLIKHMPQAAGRKNQYQGSAHVSVLDDKDDL
                                                                                                                                                                                     μ
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                                                                                                                                                                                 MQRRCNWQI FQNLEYASEQDQAELYKFENDLI KHMPQAAGRKNQYQGSAHVSVLDDKDDL
                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                      96.3%; Score 3315; DB 6;
100.0%; Pred. No. 1.9e-265;
Live 0; Mismatches 0;
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327 214

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Sequence 5631, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hintle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
ITILE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
ITILE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
ITILE OF INVENTION WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(5205)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5651
LENGTH: 722
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Best Local Similarity
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                                                                                                                                                                                                                                                  ORGANISM: Caenorhabditis elegans
                                                                                                                                                                                                                                                                   TYPE: PRT
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                                                                                                                    NAIRAAIFIOKWYRRHOARREMORRCNWQIFQNLEYASEQDQAE-----LYKFFNDLIK 57
                                 AMABENGKGGVENGRNSPLMSALSHYAKPSLMDSEGETVKKMLEDTSPTNVDIDRNYKGP
                                                                HMPQAAGRKNQYQG--SAHVSVLDD--KDDLVEEFGDIVNAKIE------
                                                                                              STÍKSÁÍLÍÓKWYRRCEÁRLEARRRATWÓI FTALEYAGEÓDÓLKVRVWITLYDFFADVIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LDTDVILEAEADGMSVMDALYANKASLVAIFNIIDADNSGEITLDEFETAIDLLVAHMPG
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                                                                                                                                                                    Conservative
                                                                                                                                                                              37.9%; Score 1305; DB 4; Length 722; 41.6%; Pred. No. 8.3e-99;
                                                                                                                                                                  117;
                                                                                                                                                                    Mismatches
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US-10-287-226-324
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Publication No. US20040086875A1
GENERAL INFORMATION:
APPLICANT: Agee, Michele L.,
APPLICANT: Alsobrook, John P.,
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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APPLICANT:
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MacDougall, John R.,
Mezes, Peter S.
Miller, Charles E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPNVFRGGGSYFGADITASFLEXHGFRLLVRSHECKFEGYEFSHNNTCLTVFSASNYYET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KYTKRPLQTDYISQIABSIDFNKDGFIDLNELLEAFRLVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEDEFRKYDPKDSGYISISHWCKVMENVTKLGLPWRLLRDKLAP-GTDSQKVNYNRTLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSNRGAYVKFIGKSKOPHFVQYM--ASKTHRKSTLRERLGVVEESAVKELKEKLSSFHTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSNKGAYIR-LNNQLMPHFVQYISAASQTKRLS-PKQRMGIVESSALKELAVRMRDHRDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDSTSLDLIKSIDRGKYVSILRPPLTDGEPLDK-----TEWQQIFDIMWSDPQATMGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNRGNHEDHIMNLRYGFIKELSTKYKDLSTPITRLLEDVFSWLPIATIIDRDIFVVHGGI
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                                             Patturajan, Meera,
Rastelli, Luca,
Rieger, Daniel K.,
                                                                                                                                                                                                                                                                                                                       Eisen, Andrew,
Ellerman, Karen,
Gangolli, Esha A.,
Spaderna, Steven
               Rothenberg, Mark E.,
Shenoy, Suresh G.,
                                                                                              Ort, Tatiana,
Padigaru, Muralidhara,
                                                                                                                                              Millet,
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                                                                                                                                                                                                                                                                                                                                                                                           DiPippo,
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                                                                                                                                                                                                                                                                                                                                                                                                                           Chant, John
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                                                                                                                             Chean Eng,
                                                                                                                                            Isabelle,
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                                                                                                                                                                                                                                                                                              Valerie,
                                                                                                                                                                                                                                                                                                                                                                            Shlomit R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Catherine E.,
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SEQ ID NO 324
LENGTH: 613
TYPE: PRT
ORGANISM: Homo sapiens
S-10-287-226-324
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Best Local Similarity
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PRIOR
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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2001-11-30
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APPLICATION NUMBER: 60/360,148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2001-11-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/354,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/334,027
FILING DATE: 2001-11-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/364,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/404,821 FILING DATE: 2002-08-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2002-02-27
APPLICATION NUMBER: 60/364,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/334,526
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14 DTSLRAALIIQNWYRGYKARLKARQHYALTIFQSIEYADEQGQMQLSTFFSFMLENYTHI
                                                                                                                                                                                                                                                                                                                                                                             - ILHAHYVLEVLFETKKVLKQMPNFTHIQTSPSKEVTICGDLHGKLDDLFLIFYKNGLPS
                                                                                                                                                                                                                                                                                                                                                                                                NRLHPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLLVVLHKNGLPS 177
GTTPRFFQY----QVTKATCFQPLRQRVDTMENSAIKILRERVISRKSDLTRAFQLQDHR
                                     QLMPHFVQYISAASQTKRLSF---KQRMGIVESSALKELAVRMRDHRDELEDEFRKYDPK 456
                                                                                             GPDVTDNFLQRHRLSYVIRSHECKÞNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRLNN 399
                                                                                                                                                                                     IKSIDRGKYVSILRPPLTDGEP---LDKTEWQQIFDIMWSDPQATMGCVPNTLRGAGVWF 339
                                                                                                                                                                                                                                                                                                    ERNPYVFNGDFVDRGKNSIEILMILCVSFLVYPNDLHLNRGNHEDFMMNLRYGFTKEILH
                                                                                                                                                                                                                                                                                                                            SSNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNARYGFIREVES
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                                                                          GPDVTSKILNKYQLKMLIRSHECKPEGYEICHDGKVVTIFSASNYYBEGSNRGAYIKLCS
                                                                                                                                                                                                                            KYKLHGKRILQILEEFYAWLPTETNRDHGTDSKHNKVGVTFNA-----HGRIK-----
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Taupier, Jr., Raymond J.,
Vernet, Corine A.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative 115; Mismatches 200;
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                                                                                                                                                      ----TNGSPTEHLTEHEWEQIIDILWSDPRGKNGCFPNTCRGGGCYF
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            CURRENT APPLICATION NUMBER: US/10/287,226
CURRENT FILING DATE: 2002-11-04
PRIOR APPLICATION NUMBER: 60/334,421
PRIOR FILING DATE: 2001-11-30
PRIOR FILING DATE: 2001-11-30
PRIOR PRILING DATE: 2002-02-04
PRIOR PRILING DATE: 2002-02-04
PRIOR PRILING DATE: 2002-02-27
PRIOR PRILING DATE: 2002-02-27
PRIOR PILING DATE: 2002-03-13
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PRIOR PILING DATE: 2002-03-13
PRIOR PILING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: 60/334,526
PRIOR PILING DATE: 2001-11-30
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US-10-287-226-326
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APPLICANT:
APPLICANT:
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APPLICANT:
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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-480C
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APPLICANT: Alsobrook, John P.,
                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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APPLICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      459 KSGKLSVSQWAFCMENILGINLPWRSLSSNIVNIDQNGNVEYMSSFQNIRIEKPVQEAHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        457 DSGYISISHWCKVMENVTKLGLPWRLLIRDKLAPGTDSQKVNYNRTLDLLDTD-VILEAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chaudhuri, Amar Chaudhuri, Amar Chaudhuri, Amar Ainger, Shlomit R.,
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Rothenberg, Mark E.,
Shenoy, Suresh G.,
Spaderna, Steven K.,
Spytek, Kimberley A.,
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Vernet, Corine A.M.,
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Millet, Isabelle,
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Gerlach, Valerie,
                                                                                                                                                                                                                                                                                                                                                           Zerhusen, Bryan D.,
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MacDougall, John R.,
Mezes, Peter S.
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Rastelli, Luca,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Padigaru, Muralidhara,
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NUMBER: 60/354,409
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PRIOR FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: 60/364,227
PRIOR PELLING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 60/334,027
PRIOR PILLING DATE: 2001-11-29
PRIOR PILLING DATE: 2001-11-20
PRIOR FILING DATE: 2001-11-20
PRIOR OF SEG ID NOS: 673
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 326
LENGTH: 613
TYPE: PRI
TYPE: PRI
                                                        RESULT 5
US-10-425-115-347492
US-10-425-115-347492
; Sequence 347492, Application US/10425115
; Publication No. US/20040214272A1
; GENERAL INFORMATION:
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Best Local Similarity
Matches 247; Conserv
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ORGANISM: Homo sapiens
-10-287-226-326
APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua
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                                                                                                                                                                                                       NIMDLNKDGSIDFNEFLKAFYV--VHRYE 602
                                                                                                                                                                                                                                                                                                                          DGMSVMDALYANKASLVAIFNIIDADNSGEITLDEFETAIDLLVAHMPGAYSKAEMLEKC
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; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21[6322]B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 347492
; LENGTH: 483
; TYPE: PRT
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US-10-425-114-61206
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                                                                           ; OTHER INFORMATION: US-10-425-114-61206
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                                                                                                                                                                                             APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Schou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven B
APPLICANT: Tabaska, Jack B
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 61206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 61206, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 16.9%; Score 581; DB 4; Best Local Similarity 41.4%; Pred. No. 4.4e-39; Matches 127; Conservative 47; Mismatches 109;
               Query Match
Best Local Similarity
Matches
                                                                                                                    LENGTH: 488

TYPE: PRT

ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Zea mays
PEATURE:
OTHER INFORMATION: Clone ID: MRT4577_80075C.1.pep
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Conservative
                                                                                                 Clone ID: LIB3732-029-F9_FLI.pep
                 16.9%; Score 581; DB 4; Length 488; 41.4%; Pred. No. 4.5e-39;
47;
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Indels
24;
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US-11-097-143-18312
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CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR PILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-11-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR PILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR APPLICATION NUMBER: 60/184,831
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Publication No. US20050208558A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: et al.
                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 18312
LENGTH: 520
                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: DETECTION KIT, SUCH AS TITLE OF INVENTION: ARRAYS, FOR DETECTING TITLE OF INVENTION: DROSOPHILA GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: CL000728
                                                                                                                                                                                                                                                                                                                       ORGANISM: DROSOPHILA
                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 MNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGG-FS-DSTSLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
     167
                                                                                                 108
                                                                                                                                                                                                  136;
                                                   58
                                                                                                                                            4 NAIRA-AIFIQKWYRRHQARREM----QRRCNWQIFQNLEYASEQDQAELYKFFNDLIK-
RAFERAIAVDKPEKT-LSEMYSDMENITIEDDYKGPQLED-----GKVTLKFMKE----
                                                                                                 SAVKADPAYLKGYYRRAAAHMSLGKFKQALCDFEFVAKCR-PNDKDAKLKFTECNKIVKM 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MPHFVQY 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IKSIDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMGCVPNTLRGAGVWFGPD 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLLNIFDLNGLPSEENPYLFNGDFYDRGSFSVEVILTLFAFKCLYPKAMYLARGNHESKS 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLLVVLHKNGLPSSSNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSV 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VKAMLDEFKKOK--CIHKRYAYQIVLKTLDLLRSMPSLVDVDVPNGGHFTVCGDVHGQYF 238
                                             -----HMPQAAGRKNQYQGSAHVSVLDD-KDDLVEEFGDIVNAKIELPIRKNHIDL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VTDNFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNYVAIGSNKGAYIRLN-NQL 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MNKIYGPEGEVRSKLGEKFVELFA---EVFCWLPLAHVINNKVFVVHGGLFSVDGVKLSD 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDLLIDVFRKKRGNRLHPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLD 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VTXKFLQENNLDLIVRSHEVKDEGHEIEHDGKLITVFSAPNYCDQMGNKGAFIRFTAPEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IRSIDR-----FCEPP------EEGLMCELLWSDPQPQLGRGPSK-RGVALSFGAD
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                   16.8%; Score 577; DB 6; Length 520; 32.1%; Pred. No. 1.1e-38;
                                                                                                                                                                                               83;
                                                                                                                                                                                            Mismatches 153; Indels 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEIC ACID
EXPRESSION OF 10,000 OR MORE
                                                                                                                                                                                            Gaps
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; FRATURE:
; NAME/KBY: misc feature
; LOCATION: (1)...(500)
; OTHER INFORMATION: Xaa = X
US-10-450-763-40348
                                    δ
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US-10-450-763-40348
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CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: CT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 40348, Application US/10450763

Publication No. US20050196754A1

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INCENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 60736
SOPTWARE: CLUSTOM
SEQ ID NO 40348
LENGTH: 500
TYPE: PRT
                                                                                     Matches
                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
FEATURE:
PRATICE: DOMAIN
LOCATION: (405)...(460)
OTHER INFORMATION: Serine/threonine specific protein phosphatases proteins
OTHER INFORMATION: domain identified by eMATRIX, accession number BL00125D,
OTHER INFORMATION: 7.517e-37, raw score of 33.11
                                                                                                                                                                                                                                                                                  NAME/KEY: DOMAIN
LOCATION: (207)...(468)
OTHER INFORMATION: Ser/Thr pr
OTHER INFORMATION: accession
                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 LMEHYKAQK--RLHRKFAYKILCEIDTYMRAQPSLVDITVPDEEKFTICGDIHGQFYDLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 LIDVFRKKRGNRLHPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  405 FVQY 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                435 KFCKDNNLDYIIRSHEVKDMGYEVAHNGKCITVFSAPNYCDTMGNMGAFITITGNNLKPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     346 NFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRL-NNQLMPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 MYGFTGEVTAKYT---SAMADIFTQVFNWLFLCHCINQKILVMHGGLFSTEDVTLDHIRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 RYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGF--SDSTSLDLIKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274 NIFEINGLESEKNEYLFNGDEVDRGSFSVECIFTLEGEKLLYENHEFLARGNHESINMNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 VVLHKNGLPSSSNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNA
99 YIMGYYRRAASNMALGKERAALRDYETVVKVKPHDKDAKMKYQECNKIVK--PKAFER--
                                         11 FIOKWYRRHOARREMOR-RCNWQIFQNLEYAS--BODQAELYKFFNDLIKHMPQAAGRKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IERN-----COPP------BEGLMCELLWSDPQQWMG-LGQSKRGVGIQFGPDVTE
                                                                                     Conservative
                                                                                                                                                                                                                                                                                    Ser/Thr protein phosphatase domain identified by PPam, accession name STphosphatase, E-value=1.4e-106, PPam
                                                                                                          16.6%;
                                                                                                                                                                                                 or
*
                                                                                73;
                                                                                   Score 571; DB 5;
Pred. No. 3.1e-38;
3; Mismatches 153
                                                                                                                                                                                               as defined in Table
                                                                                     153;
                                                                                                                          Length 500;
                                                                                     Indels
                                                                                     42;
                                                                                     Gaps
                                                                                                                                                                                                                                                                                       PFam score of
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TYPE: PRT

ORGANISM: Oryza sativa

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT4530_91460C.1.pep

US-10-437-963-195520
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US-10-437-963-195520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Barbazuk, Brad
APPLICANT: Burbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION UNMERR: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 195520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 195520, Application US/10437963 Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                              188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
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    238
                                                  247
                                                                                           178 SSNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNARYGFIREVES
                                                                                                                                                                                     118 NRLHPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLLVVLHKNGLPS
                                                                                                                                                                                                                                     129 KIRFEBAISVGDEEKRSVADSIDYRIIEVEPQYTGPRVDGDTITLDFVKAMLDEFEKQK- 187
                                                                                                                                                                                                                                                                                                                                   77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89
                                                                                                                                                                                                                                                                                   68 QYQGSAHVSVLDDKDDLVEEFGDIVNAKIEL-----PIRKNHIDLLIDVFRKKRG 117
                                                                                                                                                                                                                                                                                                                                                                          9 AIFIQKWYRRHQARREMQR-RCNWQIFQNLEYASEQDQAELYKFFNDLIKHMPQAAGRKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cao, Yongwei
Wu, Wei
Boukharov, Andrey A
Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHEVKAEGYEVAHGGRCVTVFSAPNYCDQMGNKASYIHLQGSDLRPQFHQF 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTDGEPLDKTEWQQIFDIMWSDPQATWGCVPNTLRGAGVWPGPDVTDNFLQRHRLSYVIR 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGF--SDSTSLDLIKSIDRGKYVSILRPP 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLLVVLHKNGLPSSSN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AIAGDEHKRSVVDSLDIESMTIEDEYSXPKLEDGKVTISFMKE----LMQWYKDQK--KL 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --DSGPM-----CDLLWSDPQPQNG-RSISKRGVTCQFGPDVTKAFLEENNLDYIIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---AQMYELFSEVFEWLPLAQCINGKVLIMHGGLFSEDGVTLDDIRKIERNR-----QPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNARYGFIREVESKYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HRKCAYQILVQVKEVLSKLSTLVETTLKETEKITVCGDTHGQFYDLLNIFELNGLPSETN 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QYQGSAHV-SVLDDKD-----DLVEBFG--DIVNAKIELPIRKNHIDLLIDVFRKKRGNRL
  KYPRNHKRILAFID---EVYRWLPLGSVLNSRVLIVHGG-FS-DSTSLDLIKSIDRGKYV
                                                EENPYLFNGDFVDRGSFSVEVILTLFAFKCLYPTGMYLARGNHESKSMNKIYGFEGEVRS
                                                                                                                                            -CIHKRYAYQIVLQTVQLLRSVPSLVDVNVPDGSHFTVCGDVHGQYFDLLNIFKLNGLPS
                                                                                                                                                                                                                                                                                                                                 ARYSKGYYRRGAAYLAMGKFKEALKDFQQVKRISPNDP-----DATRKLKECEKAVQ 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRL-NNQLMPHFVQY 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYIFNGDFVDRGSFSVEVILTLFGFKLLYPDHFHLLRGNHETDNMNQIYGFEGEVKAKYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                16.6%; Score 570.5; DB 4; 34.8%; Pred. No. 3.3e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                             69; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                             49;
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                              237
                                                                                                                                            246
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US-10-732-923-9610
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US-10-043-487-296
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APPLICANT: Edgerton, Michael D
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSCENIC PLANTS WITH
FILE REFERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-04
PRIOR FILING DATE: 2002-12-04
                                                                                         Sequence 296, Application US/10043487 Publication No. US20030055220A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 140; Conserv
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SEQ ID NO 9610
LENGTH: 485
TYPE: PRT
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APPLICANT: HYBRIGENICS
APPLICANT: Pierre, LEG
TITLE OF INVENTION: Pro
TITLE OF INVENTION: ma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSRYLIVHGG-FS-DSTSLDLIKSIDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDP 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLYLAFPNAVFLNRGNHEDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVL
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Protein-protein interactions between Shigella Flexneri polypeptid mammalian polypeptides
                                             LEGRAIN
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                                                                                 SEQ ID NO 9609
LENGTH: 556
TYPE: PRT
CRGANISM: Lycopersicon esculentum
US-10-732-923-9609
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US-10-732-923-9609
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US-10-043-487-296
                                                                                                                                                                                 Sequence 9609, Application US/10732923

Sequence 9609, Application US/10732923

Publication No. U320050108791A1

GRMERAL INFORMATION:

APPLICANT: Edgerton, Michael D

TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

FILE REPERENCE: 38-15 (52796) C

CURRENT APPLICATION NUMBER: US/10/732,923

CURRENT FILING DATE: 2003-12-10

PRIOR APPLICATION NUMBER: 10/310,154

PRIOR FILING DATE: 2002-12-04

NUMBER OF SEQ ID NOS: 24149
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SEQ ID NO 296
LENGTH: 494
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Best Local :
                                           Query Match
    Matches 130;
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/261,130
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 561
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                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRYLIVHGGF--SDSTSLDLIKS 285
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    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    408
16.4%; Score 565; DB 5; Length 556; 40.2%; Pred. No. 1.2e-37; ative 47; Mismatches 114; Indels
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  32;
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; NUMBER OF SEQ ID NOS: 28
; SOFTMARE: PATENTIN Ver. 2.1
; SEQ ID NO 27
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Lycopersicon esculentum
US-10-298-638-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 16.3%; Score 562.5; DB 4; Best Local Similarity 35.8%; Pred. No. 1.5e-37; Matches 139; Conservative 55; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: HARING, Michel A. et al.

TITLE OF INVENTION: NUCLECTIOE SEQUENCES CODING SIGNAL TRANSDUCTION
TITLE OF INVENTION: COMPONENTS IN DURABLE AND BROAD-RANGE RESISTANCE
TITLE OF INVENTION: STRATEGIES BASED ON PLANT DEFENCE
FILE REFERENCE: 2121-0167P
CURRENT FAPELICATION NUMBER: US/10/298,638
CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: 10/298,638
PRIOR APPLICATION NUMBER: 10/298,638
PRIOR PILING DATE: 2002-11-19
322 QATMGCVENTLRGAGVWFGPDVTDNFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSA
                                                                                                                                                                                                                                                                                 144 PVSTAVSQQVTVCGDLHGKLDDLLVVLHKNGLPSSSNPYVFNGDFVDRGKRGLEVLLLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            512 QMGNKGAFIRFEAPDMKPNIVTF 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          387 IGSNKGAYIRLN-NQLMPHFVQY 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    408 VVHGGLFSVDGVKLSDIRAIDR----FCEPP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              351 CPSAIHLARGNHESKSMNKIYGFEGEVRSKLSEIFVELFA---EVFCCLPLAHVINEKVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 FPNAVFLNRGNHEDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291 EGKHFTVCGDVHGQFYDLLNIFBLNGLPSEDNPYLFNGDFVDRGSFSLEVILTLFAFKCM 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 VSQQVTVCGDLHGKLDDLLVVLHKNGLPSSSNPYVFNGDFVDRGKRGLEVLLLLLSLYLA 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
                                                                                                                                                                                                                                                                                                                                                                                           84 LVEEFGDIVNAKIELPIRKNHIDLLIDVFRKKRGNRLHPKYVALILREAAKSLKQLPNIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 EMORRCHWQIFQNLEYASEQDQABLYKFFNDLIKHMPQAAGRKNQYQGSAHVSVLDDKDD
                                                                                                                 NSRVLIVHGG-FS-DSTSLDLIKSIDRGKYVSILRPPLTDGBPLDKTEWQQIFDIMWSDP
                                                                        NEKVFVVHRGLPSVDGVKLSDIRAIDR-----FCEPP
                                                                                                                                                               AFKCMCPSAIHLARGNHESKSMNKIYGFEGEVRSKLSEIFVELFA---EVFCCLPLAHVI
                                                                                                                                                                                                        SLYLAFPNAVFLNRGNHEDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVL
                                                                                                                                                                                                                                                         DIVVPEGKHFTVCGDVHGQFYDLLNIFELNGLPSEDNPYLFNGDFVDRGSFSLEVILTLF
                                                                                                                                                                                                                                                                                                                                                -----GDVVTL-----DFVKKMLDDFKNQK--NLHKRYAYQIVLQTREMLRALPSLV
                                                                                                                                                                                                                                                                                                                                                                                                                                         ESORR---SVADSIDYRS------VEVEPOYAGARIE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RGPSK-RGVGLSFGGDVTKRFLQENNLDLVVRSHEVKDEGYEIEHDGKLITVFSAPNYCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CVPNTLRGAGVWFGPDVTDNFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNYYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IVHGG-FS-DSTSLDLIKSIDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDVVTL-----DFVKKMLDDFKNQK--NLHKRYAYQIVLQTRBMLRALPSLVDIVVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDIVNAKIBLPIRKNHIDLLIDVFRKKRGNRLHPKYVALILRBAAKSLKQLPNISPVSTA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 482;
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                                                                        BEGLMCELLWSDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69;
                                                                                                                                                               328
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Sequence 10, Application US/10298638

Publication No. US20030177527A1

GENERAL INFORMATION:
APPLICANT HARING, Michel A. et al.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING SIGNAL TRANSDUCTION
TITLE OF INVENTION: COMPONENTS IN DURABLE AND BROAD-RANGE RESISTANCE
TITLE OF INVENTION: STRATEGIES BASED ON PLANT DEFENCE
TITLE OF INVENTION: STRATEGIES BASED ON PLANT DEFENCE
FILE REFERENCE: 2121-0167P
CURRENT APPLICATION NUMBER: US/10/298,638
CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: 10/298,638
PRIOR FILING DATE: 2002-11-19
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 485
TYPE: PRT
CORGANISM: Lycopersicon esculentum
US-10-298-638-10
                                                                                                                                                                                                RESULT 15
US-10-424-599-191442
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US-10-298-638-10
                                                                                    Sequence 191442, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 139; Conserv
    APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic
TITLE OF INVENTION: Plants and
                                                                                                                                                                                                                                                                                                                            382
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                                                                                                                                                                                                                                                                                                               SNYYAIGSNKGAYIRLN-NQLMPHFVQY 408
                                                                                                                                                                                                                                                                                                                                                                                                   QATMGCVPNTLRGAGVWFGPDVTDNFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEKVFVVHRGLFSVDGVKLSDIRAIDR----FCEPP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSRVLIVHGG-FS-DSTSLDLIKSIDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AFKCMCPSAIHLARGNHESKSMNKIYGFEGEVRSKLSEIFVBLFA---EVFCCLPLAHVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLYLAFPNAVFLNRGNHEDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIVVPEGKHFTVCGDVHGQFYDLLNIFELNGLPSEDNPYLFNGDFVDRGSFSLEVILTLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GDVVTL------DFVKKMLDDFKNQK--NLHKRYAYQIVLQTREMLRALPSLV 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVBBFGDIVNAKIBLPIRKNHIDLLIDVFRKKRGNRLHPKYVALILRBAAKSLKQLPNIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BSQRR---SVADSIDYRS------VBVBPQYAGARIB------
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                                                                                                                                                                                                                                                                                    PNYCDQMGNKGAFIRFEAPDMKPNIVTF 463
                                                                                                                                                                                                                                                                                                                                                                      QPQPGRGPSK-RGVGLSFGGDVTKRFLQENNLDLVVRSHEVKDEGYEIEHDGKLITVFSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNYYAIGSNKGAYIRLN-NQLMPHFVQY 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMORRCNWQIFQNLEYASEQDQABLYKFFNDLIKHMPQAAGRKNQYQGSAHVSVLDDKDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.3%; Score 562.5; DB 4; 35.8%; Pred. No. 1.5e-37; tive 55; Mismatches 125;
    Acid Molecules and Other Molecules Associated Uses Thereof for Plant Improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----BEGLMCELLWSDP
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                          With
                                                                                                                                                                                                                                                                       RESULT 16
US-10-298-638-28
US-10-298-638-28
Sequence 28, Application US/10298638
Publication No. US20030177527A1
GENERAL INFORMATION:
GENERAL INFORMATION: MICHEO A. et al.
TITLE OF INVENTION: COMPONENTS IN DURABLE AND BROAD-RANGE RESISTANCE TITLE OF INVENTION: STRATEGIES BASED ON PLANT DEFENCE
TITLE OF INVENTION: USACTION DURABLE AND BROAD-RANGE RESISTANCE
TITLE OF INVENTION: USACTION DURABLE ON PLANT DEFENCE
TITLE REFERENCE: 2121-0167P
CURRENT APPLICATION NUMBER: US/10/298,638
PRIOR APPLICATION NUMBER: 10/298,638
PRIOR PILING DATE: 2002-11-19
PRIOR PILING DATE: 2002-11-19
NUMBER OF SEQ ID NOS: 28
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                                                                                                                                                      US-10-298-638-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 191442
LENGTH: 482
                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. SEQ ID NO 28
                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
                                                                  Matches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                          ORGANISM: Arabidopsis thalians
                                                                                                                                                                                              LENGTH: 533
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: unsure
LOCATION: (1)..(48:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Glycine FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 LHKRYAPQIVLQTKRXLQALPSLVDIHVPDGKHFTVCGDVHGQYYDLLNIFELNGLPSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60
LHPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLLVVLHKNGLPSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RSHEVKDEGYEIEHDGKLITVFSAPNYCDQMGNKGAFIRFEAPDLKPNIVTF 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRLN-NQLMPHFVQY 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NPYLFNGDFVDRGSFSLEVILTLFAFKCMSPSAIYLARGNHESKSMNKIYGFEGEVRSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NPYVENGDEVDRGKRGLEVILLILISIYLAFPNAVFLNRGNHEDSVMNARYGFIREVESKY 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PQAAGRKNQYQGSAHVSVLDDKDDLVBBFGDIVNAKIBLPIRKNHIDLLIDVFRKKRGNR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLTDGEPLDKTEWQQIFDIMWSDPQATMGCVPNTLRGAGVWFGPDVTDNFLQRHRLSYVI 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NETFVELFA---EVFCCLPLAHVINEKVFVVHGGLFSVDGVKVSDIRSINR----FCEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGG-FS-DSTSLDLIKSIDRGKYVSILRP
                                                                  Conservative
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                                                              16.2%; Score 557.5; DB 4; 39.4%; Pred. No. 4.6e-37; tive 55; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.3%; Score 561; DE 38.4%; Pred. No. 2e-3 tive 46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2e-37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119;
                                                                Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                        Length 533;
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                                                                Gaps
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION SUMMERS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/03-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 22595
LENGTH: 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Schizosaccharomyces pombe US-10-369-493-22595
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Best Local Similarity
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HDNKITTIFSASNYYAIGSNKGAYIRLNNQLMPHFVQY 408
                                                                                                                                                        TFSLLPLGSLISDSYLVVHGGLFSDDNVTLDQLRNIDRFS----KKQPGQSG-----
                                                                                                                                                                                               VYRWLPLGSVLNSRVLIVHGGF--SDSTSLDLIKSIDRGKYVSILRPPLTDGEPLDKTEW
                                                                                                                                                                                                                                            SWSTEVAFTLYAYKLLYPDAVFINRGNHETDDMNKVYGFEGECRSKY---NERTFNIFSE
                                                                                                                                                                                                                                                                                                                                  KELLEKTPSLIDIPVKGDETLVICGDTHGQYFDLLNIFKLHGPPSPTNKYLFNGDFVDRG
                                                                 - LMMEMLWTDPQPAPGRGPSK-RGVGLQFGPDVSKRFCEANGLKAVIRSHEVRDQGYEVE
                                                                                                             QQIFDIMWSDPQATMGCVPNTLRGAGVWFGPDVTDNFLQRHRLSYVIRSHECKPNGHEFM 370
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Stater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION STATES
PRIOR FILING DATE: 2002-02-21
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    RESULT 19
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SEQ ID NO 4091
LENGTH: 598
TYPE: PRT
ORGANISM: Neurospora crass.
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Publication No. US20030233675A1
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NAME/KEY: unsure
LOCATION: (1)..(598)
OTHER INFORMATION: U
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                                                                                                             406 VQY 408
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                                                                                                                                                                                                                                                                            IDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMGCVPNTLRGAGVWFGPDVTD
                                                                                                                                                                                                                                                                                                                            PEHTPADTSHLLPRTYK----LFSESFSALPLATLIGKKFLVLHGGLFSDDNVTLDDIRK 478
                                                                                                                                                                                               NFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRLNNQLMPHF
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                                                                 SQF 587
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FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-09-33
PRIOR PILING DATE: 2000-09-33
NUMBER OF SEQ ID NOS: 60736
SEQ ID NO 40347
LENGTH: 714
            RESULT 20
US-10-369-493-21980
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; OTHER INFORMATION: Ser/Thr protein phosphatase domain identified by PFam,
; OTHER INFORMATION: accession name STphosphatase, B-value=4.6e-92, PFam score of 319
US-10-450-763-40347
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Publication No. US20050196754A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 140; Conserv
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OTHER INFORMATION: SERINE/THREONINE PHOSPHATASE FAMILY SIGNATURE domain OTHER INFORMATION: identified by eMATRIX, accession number PR00114A, p-v-OTHER INFORMATION: 25, raw score of 14.44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---DLVEBFG--DIVNAKIBLPIRKNHIDLLIDVFRKKRGNRLHPKYVALILREAAKSLK 137
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                                                                                                                                                                                                    LGPVHLLHGAVMASTVVTMVRGEGTVTAEHTCPYLFNGRSISKRGVSCQFGPDVTKAFLE
                                                                                                                                                                                                                                                                                              HIGGLESEDGVTLDDIRKIERNR-----QPP--DSALPRRMGFVPLARNSGSEPQFPHLR
                                                                                                                                                                                                                                                                                                                                                  VHGGF--SDSTSLDLIKSIDRGKYVSILRPPLTDG8PLDKTEWQQIFDIMWSDPQ-----
                                                                                                                                                                                                                                                                                                                                                                                                 PDHFHLLRGNHETDNMNQIYGFEGEVKAKYT---AQMYELFSEVFEWLPLAQCINGKVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                            PNAVFLNRGNHEDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POPOVCTEWEEPLPGKDVTLERRGLAMLGHQGQIFNGDFVDRGSFSVEVILTLFGFKLLY
                                                                                                                                                     RHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRL-NNQLMPHFVQY
                                                                                                                                                                                                                                                      ----ATMGCVPNTL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.4%; Score 496.5; DB 5; 29.2%; Pred. No. 8e-32;
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Sequence 5986, Application US/11097143
Publication No. US20050208558A1

GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: Venter, J. Craig
APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUTTITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION NUMBER: US/11/097,143
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
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RESULT 21
US-11-097-143-5988
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TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B (10/369,493)
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 21980
LENGTH: 513
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                   380
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                                                                                                                                                                                                                                                                                                                        237
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                                                                                                                                                                                                                           LRPPLTDGEPLDKTEWQQIFDIMWSDPQATMGCVPNTLRGAGVWFGPDVTDNFLQRHRLS
                                                                                                                                                                                                                                                                                                               SKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGF-SD-STSLDLIKSIDRGKYVSI
                                                                                                                                                                                                                                                                                                                                                                                                SSSNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNARYGFIREVE
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                                                                                      KIFRSHELRMGGVQFEQKGKLMTVFSAPNYCDSQGNLGGVIHV
                                                                                                                                                                                   AQPP-RDG-----AFMELLWADPQEANGMGPSQ-RGLGHAFGPDITDRFLRNNKLR 428
                                                                                                                                                                                                                                                                           YKY---SQRIFNMFAQSFESLPLATLINNDYLVMHGGLPSDPSATLSDFKNIDR-----F
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NUCLEIC ACI

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10,000 OR MORE

Gaps

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Sequence 13007, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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                                       ; TYPE: PRT
; ORGANISM: Aspergillus nidulans
US-10-369-493-13007
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US-11-097-143-5988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR PILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR PILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR PILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
                                                                                              APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION (TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/360,039
PRIOR APPLICATION NUMBER: US/360,039
PRIOR APPLICATION NUMBER: US/360,039
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NO 13007
LENGTH: 244
THE TRANSPORT OF SEQ ID NOS: 47374
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PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5988
    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HESADLNRVYGFFDECKRRY--SIKLWRSFVD-CYDCMPVAAIIADRIFCVHGGLSPDLN 196
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    13.1%;
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Pred. No. 2.6e-29;
    Score 451;
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  Length 244;
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 225312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Clone ID: MRT4577_137074C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPB: PRT
ORGANISM: Zea mays
FEATURB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 443
                                                                                                         324 TMGCVPNTLRGAGVWFGPDVTDNFLQRHRLSYVIRSHECKPNGHEFMHD------
                                                                                                                                                250
                                                                                                                                                                                                                                                                           240
                                                                                                                                                                                                                                                                                                                   134 RIFVFNGDYVDRGAWGLETFLLLLAWKVLLPNCVFLLRGNHESKYCTSVYGFEKEVMTKY
                                                                                                                                                                                                                                                                                                                                                        180 NPYVFNGDFVDRGKRGLEVLILLISLYLAFFNAVFLNRGNHEDSVMNARYGFIREVBSKY 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   397
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                                                                                                                                                                                                                                                                                                                                                                                                                                            120 LHPKYVALILRBAAKSIKQIPNISPVSTAVSQQVTVCGDIHGKIDDILVVIHKNGIPSSS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222 IGPELKLEYQVFEAVPH 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279
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                                                                                                                                                                                                                                                                                                                                                                                                    74 LPPALVQRLVLAAAAILHREPNLVRVDPRPGQAVVVVGDVHGQLHDVIFLLRDAGFPSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98; Conservative
----NKIITIFSASNYYAIG-----SNKGAYIRLN 398
                                                                                                                                                KANPTVDLTSMKLGSLDELLKARRTVLDPPWEGSNLIPG------DVLWSDPSL 297
                                                                                                                                                                                                                               KDQGPQIYRKFLRCFED----LPLATIIAGCVYTAHGGIFRGTIVVPSKKSKKGKKGHKY 249
                                                                                                                                                                                                                                                                       ----PRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGFSDSTSLDLIKSIDRGK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LQFGPDVTKRFCENNGLEAIIRSHEVRMNGYEVEHDGRCITVFSAPKYCDTTENKGAFIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VWEGEDVTDNELQRHRLSYVIRSHECKENGHEFMHDNKIITIFSASNYYAIGSNKGAYIR 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLDDIRKLNRHN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLDLIKSIDRGKYVSILRPPLTDGEPLDKTEWQQ--IFDIMWSDPQATMGCVPNTLRGAG 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETDDMNKVYGPEGECRAKY---NETMPKVPSESPSALPLATLIGNKYLVLHGGLFSDDKT
                                                               QMGLSPNKERGIGLLWGPDITQQFLRTNHLKLIIRSHE-GPDARDKRHDLLGMDKGYTID 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GOFFDLLEIFRLNGFPSDTHAYLFNGDFVDRGSWSTEIALLLYAYKWLRPNGIFLNRGNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.0%; Score 447.5; DB 4
33.5%; Pred. No. 4.5e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 404
                                                                                                                                                                                      ---YVSILRPP----LTDGEPLDKTEWQQIFDIMWSDPQA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 9.3e-29;
3; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -QKQPGQQGLMMEMLWTDPQTEPGRGPSK-RGVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Other Molecules Associated With
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 443;
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US-10-425-114-50385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/317,305
PRIOR FILING DATE: 2001-09-05
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 20
LENGTH: 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20, Application US/10236699
Publication No. US20030150028A1
GENERAL INFORMATION:
APPLICANT: BOHNERT, HANS J.
APPLICANT: CHEN, RUOYING
APPLICANT: ISHITANI, MANABU
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack B
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                       Sequence 50385, Application US/10425114 Publication No. US20040034888A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local 9
                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: VAN THIELEN, NOCHA
APPLICANT: COSTA E SILVA, OSWALDO DA
TITLE OF INVENTION: PROTEIN PHOSPHATASE STRESS-RELATED POLYPEPTIDES
TITLE OF INVENTION: METHODS OF USE IN PLANTS
FILE REFERENCE: 16313-0161
CURRENT APPLICATION NUMBER: US/10/236,699
CURRENT FILING DATE: 2002-09-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             269 IVHGGFS-DSTSLDLIKSIDRGKYVSILRPPLTDGEPLDKTEMQQIFDIMWSDPQATMGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 YPENFFLLRGNHECASINRIYGFYDECKRRF---NVRLWKTFTDCFNCLFVAALVDEKIL
                                                                                                                                                                                                                                                                                                                                                                                                                             272 FDNAGAMMSVDETLMCSF-QILKPADKKAKLNF 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 IK----ICGDVHGQYSDLLRLFEYGGLPPEAN-YLFLGDYVDRGKQSLETICLLLAYKIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 DIVNAKIELP-IRKNHIDLLIDVFRKKRGNRLHPKYVALILRBAAKSLKQLPNISPVSTA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSQQVTVCGDLHGKLDDLLVVLHKNGLPSSSNPYVFNGDFVDRGKRGLEVLLLLLSLYLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIINRLLEVPTLPAKQVQLSESEIRQ-----LCVVSREI---FLQQPNLLELEAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSNKGAYIRLMNQLMPHFVQYISAASQTKRLSF 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WGMNDRGVSYTFGADKVSQFLQKHDLDLVCRAHQVVEDGYEFFANRQLVT1FSAPNYCGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.7%; Score 435.5; DB 4; 31.2%; Pred. No. 2.7e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----PTDVPDTGLLCDLLWSDPSKDVQG
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US-10-424-599-254277
; Sequence 254277, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
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US-10-424-599-254277
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SEQ ID NO 50385
LENGTH: 339
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SEQ ID NO 254277
LENGTH: 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                              Matches 105;
                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
PILE REFERENCE: 38-21 (53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: La Rosa Thomas
APPLICANT: Kovalic David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Glycine max
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 YPPAST-YVFLGDYVDRGKQSLETICLLLAYKIRYPENIFLLRGNHEDAKINRVYGFYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 LPSSSNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNARYGFIRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 DLICRAHQVVEDGYEFFAQRRLVTIFSAPNYCGEFDNVGALLSIDESLMCSF 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354 SYVIRSHECKPNGHEFWHDNKIITIFSASNYYAIGSNKGAYIRLNNQLMPHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 CKRRF---NVRLWKIFSDCFNCLPIAALIDDKILCMHGGLSPELTSLDQIKDIER----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235 VESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGFS-DSTSLDLIKSIDRGKYVS
                                       136 LKQLPNISPVSTAVSQQVTVCGDLHGKLDDLLVVLHKNGLPSSSNPYVFNGDFVDRGKRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 GROVOLSEABIROLCVEGKRVLLSOPNL----LRIHAPVKICGDIHGQFVDLLRLFDLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 IKHMPQ-AAGRKNQYQGSAHVSVLDDKDDLVBEFGDIVNAKIBLPIRKNHIDLLIDVFRK 114
42 FLOOPNILEIEAPIK----ICGDVHGQYSDLLRIFEYGGLPPEAN-YLFIGDYVDRGKQS
                                                                                                                               76 SYLDDKDDLYBBFGDIVNAKIBLPIRKNHIDLLIDVFRKKRGNRLHPKYVALILRBAAKS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILRPPLIDGEPLDKTEWQQIFDIMWSDPQATMGCVPNTLRGAGVWFGPDVTDNFLQRHRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KRGNRLHPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLLVVLHKNG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRHTPRPSPGRK---EGGGKWMTR-----APMGPMEGAAVDEMVRR-----LVEGGRG 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kovalic David K
                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.6%; Score 434.5; DB 4; Length 339; 30.1%; Pred. No. 3.6e-27; tive 72; Mismatches 135; Indels 39;
                                                                                                                                                                                                 12.6%;
                                                                                      DIINRLLEVRTRPG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID: LIB3062-002-C7_FLI.per
                                                                                                                                                                              69; Mismatches
                                                                                                                                                                                                 Score 432.5; DB 4
Pred. No. 4.9e-27;
                                                                                      ----KQVQLSESBIRQLCVVSREI----
                                                                                                                                                                                                                      DB 4; Length 326;
                                                                                                                                                                              125,
                                                                                                                                                                              Indels
                                                                                                                                                                              47;
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                                            195
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APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven B

APPLICANT: Tabaska, Jack B

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPERBENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

SEQ ID NO 65099

LENGTH: 380

TYPB: ppm
   RESULT 28
US-10-739-930-9917
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Best Local S
Matches 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y Match 12.5%;
Local Similarity 30.5%;
nes 102; Conservative 60
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                                                                                                                                           265
                                                                                                                                                                            327
                                                                                                                                                                                                               220
                                                                                                                                                                                                                                        268 LIVHGGFS-DSTSLDLIKSIDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMG
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                                                                                                                                                                                                                                                                                  163 KYPENFFLLRGNHECASINRIYĞFYDECKRRF---NVRLWKTFTECFNCLFVAALIDEKI
                                                                                                                                                                                                                                                                                                                                                                                    148 AVSQQVTVCGDLHGKLDDLLVVLHKNGLPSSSNPYVFNGDFVDRGKRGLEVLLLLLSLYL 207
                                                                                                                                                                                                                                                                                                                                                                                                                          62
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                                                                      EFDNAGAMMSVDETLMCSF-QILKPADKKAKLNF 357
                                                                                                       IGSNKGAYIRLNNQLMPHFVQYISAASQTKRLSF 420
                                                                                                                                                                          CVPNTLRGAGVWFGPDVTDNFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNYYA 386
                                                                                                                                                                                                                                                                                                               AFPNAVFLNRGNHEDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRV
                                                                                                                                                                                                                                                                                                                                                   PIK----ICGDVHGQYSDLLRLFEYGGLPPEAN-YLFLGDYVDRGKQSLETICLLLAYKI 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVTÍFSAPNYCGBFDNAGAMMSVDETLMCSF-QILKPADKKAKLNF 303
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                                                                                                                                        GWGWNDRGVSYTFGADKVSEFLOKHDLDLICKAHOVVEDGYEFFANROLVTIFSAPNYCG 324
                                                                                                                                                                                                           LCMHGGLSPDILNLDQIRNLQR------PTDVPDTGLLCDLLWSDPSKEVQ 264
                                                                                                                                                                                                                                                                                                                                                                                                                       DIINRLLEV------RSRPGKQVQLSESEIRHLCAASREIFLQQPNLLELEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 431.5; DB 4;
Pred. No. 7.5e-27;
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Query Match
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                                                                     FEATURE:
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; OTHER INFORMATION: Clone ID: US-10-425-114-64475
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US-10-425-114-64475
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                                                                                                                                              GENERAL INFORMATION:

APPLICANT: Liu, Jingdong
APPLICANT: Chou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLS REFERENCE: 38-21(53)13)B
FULS REFERENCE: 38-21(53)13)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 64475
LENGTH: 334
TYPER: DET
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NUMBER OF SEQ ID NOS: 11088

SEQ ID NO 9917

LENGTH: 325

TYPE: PRT

ORGANISM: Triticum aestivum

PEATURE: TRECOMMETON: Color ID TEXTER CARDO CO. 225
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Publication No. US20040034888A1
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Publication No. US20040216190A1
GENERAL.INFORMATION:
APPLICANT: Kovalic, David K.
                                                                                           TYPE: PRT
ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221 WGESDRGVSCTFGADMLIEFLEKNDLDLICRAHQVVEDGYEFFAQRRLVTIFSÅPNYCGE 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      328 VPNTLRGAGVWFGPDVTDNFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNYYAI 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   269 IVHGGFS-DSTSLDLIKSIDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMGC 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209 FPNAVFLNRGNHEDSVMNARYGFIREVESKYFRNHKRILAFIDEVYRWLFLGSVLNSRVL 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281 FDNVGALLSIDENLMCSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CMHGGLSPELTNLDQIKDIER-----PABIPDYGLLCDLLWSDPSPDGEG 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAMEGAALDEVVRR-----LVEGGRGGRQVQLSBABIRQLCVDAKRVFLSQPNL----LR 59
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                              LIB3969-010-E2_FLI.pep
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12.5%;

Score 430.5;

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Length 334;

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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Tabaska, Jack B
APPLICANT: Tabaska, Jack B
APPLICANT: Tabaska, Jack B
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
INVMBER OF SEQ ID NOS: 73128
SEQ ID NO 70117
LENGTH: 334
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US-10-425-114-70117
                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: UC-ZMFLMO17236G06_FLI.pep
US-10-425-114-70117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 70117, Application US/10425114 Publication No. US20040034888A1 GENERAL INFORMATION:
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Best Local &
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ORGANISM: Zea mays
FEATURE:
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                                106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RF---NVRLWKVFTECFNTLPVAALIDDKILCMHGGLSPDLAHLDBIKNLQR------
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                           EAN-YLFLGDYVDRGKQSLETICLLLAYKIKYPENFFLLRGNHECASINRIYGFYDECKR
                                                                  SSNPYVENGDEVDRGKRGLEVLLLLLSLYLAFENAVELNRGNHEDSVMNARYGFIREVES 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QIYGAKQNV 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----PTDVPDQGLLCDLLWSDPGKDVQGWGMND-RGVSYTFGADKV8EFLQRHDLDL
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                                                                                                                                                                   NRLHPKYVALILRBAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLLVVLHKNGLPS 177
                                                                                                                                                                                                                    PAAGG---QGGGGIDAALL---DDIIRRLLEVRTARPGKQVQLSESEIRQLCTVSR----
                                                                                                                                                                                                                                                                PQAAGRKNQYQGSAHVSVLDDKDDLVEBFGDIVNAK--IBLPIRKNHIDLLIDVFRKKRG
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tive 67; Mismatches 134;
                                                                                                                                                                                                                                                                                                                  67; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67;
                                                                                                                                                                                                                                                                                                                                        Score 430.5; DB 4; Pred. No. 7.5e-27;
                                                                                                                                                                                                                                                                                                                                                              Length 334;
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US-10-739-930-7415
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US-10-739-930-9330
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Best Local S
Matches 99
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TITLE OF INVENTION: NUCLEIC AGID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
PILE REPERENCE: 38-21(53377)B
CURRENT PPLLCATION NUMBER: US/10/739,930
CURRENT PILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 7415
Sequence 9330, Application US/10739930
Publication No. US20040216190A1
GENERAL IMPORMATION:
APPLICANT: Kovalic, David K.
TITLE OF INVENTION: NUCLEIC ACID MOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7415, Application US/10739930 Publication No. US20040216190A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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                                                                                                                                                                                                                    286 ALLSIDESLMCSF 298
                                                                                                                                                                                                                                                                                                                                                                                                                181 LSPELTSLDQIKDIER----
                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 FS-DSTSLDLIKSIDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMGCVPNTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 YLLRGNHEDAKINRVYGFYDECKRRF---NVRLWKIFCDCFNCLPMAALIDDKILCMHGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 TVCGDLHGKLDDLLVVLHKNGLPSSSNPYVENGDFVDRGKRGLEVLLLLLSIYLAFPNAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 KICGDIHGQEVDLLRLFDLGGYPPTST-YIFLGDYVDRGKQSLETICLLLAYKLKYPDNI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 AAVDEVVRR-----LVEGGRGGRQVQMSEABIRQLCVEAKQVLLSQPNL----LRIHAPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 AKIELPIRKNHIDLLIDVFRKKRGNRLHPKYVALILREAAKSLKQLPNISPVSTAVSQQV
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                                                                                                                                                                                                                                                                                                                  RGVSCTFGADKLVEFLEKNDLDLVCRAHQVVEDGYEFFAERRLVTTFSAPNYCGEFDNAG
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  David K. NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
                                                                                                                                                                                                                                                                405
                                                                                                                                                                                                                                                                                                                                                                                                                PTEIPDYGLLCDLLWSDPSHDTEGWGESD
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RESULT 33
US-10-425-114-62750
US-10-425-114-62750, Application US/10425114; Publication No. US20040034888A1
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US-10-739-930-9330
                                                                                                                                                                                        US-10-425-114-62750
                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 62750
LENGTH: 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (5331)B
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                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Zea mays
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ORGANISM: Glycine
FEATURE:
                                                                                                                                                                                                      OTHER INFORMATION: Clone ID: LIB3357-018-H5_FLI.pep
                                                                                                                                                                                                                                         FEATURE:
                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 AFPNAVFLNRGNHEDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRV 267
                                                                              al Similarity
103; Conserv
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94 AKIBLPIR-----KWHIDLLIDVFRKKRGNRLHPKYVALI----LREAAKSLKQLPNI 142
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Similarity 30.5%;
02; Conservative 66
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                                                                                 Conservative
                                                                                                       12.5%; Score 429; DB 4
31.8%; Pred. No. 1e-26;
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                                                                                 Mismatches
                                                                                                                             DB 4; Length 338;
                                                                                 129;
                                                                              Indels
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LENGTH: 338
TYPE: PRT
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Publication No. US20040034888A1
GENERAL INFORMATION:
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APPLICANT: Zhou, Yihua
APPLICANT: Scoten, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                            382 SNYYAIGSNKGAYIRLNNQLMPHF 405
                                                   221 DKEIDRWGENDRGVSYTFGADVVAEFLOKHDLDLICRAHQVVEDGYEFFAKRQLVTIFSA
                                                                                                    322 QATMGCVPNTLRGAGVWFGPDVTDNFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSA 381
                                                                                                                                                                                                      263 LNSRVLIVHGGFS-DSTSLDLIKSIDRGKYVSILRPPLTDGBPLDKTEWQQIFDIMWSDP
                                                                                                                                                                                                                                                            119 LAYKIKYPENFFLLRGNHECASINRIYGFFDECKRRF---NVRIWKIFTECFNCLPVAAL
                                                                                                                                                                                                                                                                                                                203 LSLYLAFPNAVFLNRGNHEDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSV 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            281 PNYCGEFDNAGALMSIDNSLVCSF 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 QATMGCVPNTLRGAGVWFGPDVTDNFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 LNSRVLIVHGGFS-DSTSLDLIKSIDRGKYVSILRPPLTDGBPLDKTEWQQIFDIMWSDP 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 LAYKIKYPENFFLLRGNHECASINRIYGFFDECKRRF---NVRIWKIFTECFNCLPVAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 LSLYLAFPNAVFLNRGNHEDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSV 262
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                                                                                                                                                                                                                                                                                                                                                                    60 QPNLLELEAPIKICGDVHGQYSDLLRLFEYGGYPPDAN-YLFLGDYVDRGKQSIBTICLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 AKIELPIR-----KNHIDLLIDVFRKKRGNRLHPKYVALI---LREAAKSLKQLPNI 142
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                                                                                                                                                        IDDKIFCMHGGLSPDLKSMDQIRNIPR------PVDVPDVGLLCDLLWSDP
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31.8%; Pred. No. 1e-26;
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_102005C.1.pep
US-10-437-963-104697
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US-10-437-963-104697
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                                                                                                                                               US-10-369-493-2574
                                                                                                                                                                        RESULT 36
           Sequence 2574, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 104697
LENGTH: 428
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Publication No. US20040123343A1
GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yongwei
APPLICANT:
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                       379 N 379
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                                                                                                                                                                                                                                                                                                                         320 HE-GPDARDKRHDLLGMDNGYTIDHHVECGKLITLFSAPDYPQFQASEDRYNNCGAYIVL
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                                                                                                                                                                                                                                                                                                                                                                  360 HECKPNGHEFMHD------NKITTIFSASNYYAIG-----SNKGAYIRL 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 PVSTAVSQQVTVCGDLHGKLDDLLVVLHKNGLPSSSNPYVFNGDFVDRGKRGLEVLLLLL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 RYDPRPDQAVVVVGDVHGQLHDVIFLLRDAGFPSDDRVFVFNGDYVDRGAMGLETFLLLL 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----TEWQQI-----FDIMWSDPQATMGCVPNTLRGAGVWFGPDVTDNFLQRHRLSYVIRS 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTIAGCVYTAHGGIFRGTIVMPSKRTKKGKKGNKYKANSSVDPTLMKLGSLDELLKARR 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTREWVAGLTATLDWCSRSLPADRLPDV-----LPAALVQRLVLAASVILHREPNLV 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boukharov, Andrey
Barbazuk, Brad
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                                                                     ; OTHER INFORMATION: Clone ID: US-10-425-115-293335
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TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-21
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEG ID NOS: 47374
SEG ID NO 2574
                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 293335
LENGTH: 322
TYPE: PRT
ORGANISM: Zea mays
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Best Local (
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Nucleic Acid Molecules
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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NAME/KEY: unsure
LOCATION: (1). (316)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                            FEATURE:
NAME/KEY: unsure
LOCATION: (1)...(322)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                FEATURE:
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Local Similarity 34.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323 ATMGCVPNTLRGAGVWFGPDVTDNFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSAS 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 DEKIFTMHGGLSPDLNSMDQIQRIMR------PTDVPDTGLLCDLLWSDPD 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KOLTGWGDNDRGVSFTFGFDVVSRFLHKHDMDLVCRAHQVVEDGYEFFSKRQLVTLFSAF
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12.4%;
30.4%;
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                                                                                      MRT4577_30602C.1.pep
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Pred. No. 1.2e-26;
Score 427.5; DB 4;
Pred. No. 1.3e-26;
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                     Length 322;
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_15395C.1.pep
US-10-437-963-111414
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SEQ ID NO 111414
LENGTH: 322
TYPE: PRT
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Best Local Similarity
Matches 114; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      356 VIRSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRLNNQLMPHFVQYISAASQT 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203
                          172 KNGLPSSSNPYVENGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNARYGF 231
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                                                                                                                             119 RLHPKYVALILREAAKSLKQLPNIS-----PVSTAVSQQVTVCGDLHGKLDDLLVVLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 KYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGFS-DSTSLDLIKSIDRGKYVSILR 296
        89
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                                                                                                                                                                                                                59 MPQAAGRKNQYQGSAHVSVLDDKDDLVEEFGDIVNAKIELPIRKNHIDLLIDVFRKKRGN 118
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                                                                                                                                                                               1 MAAAPGAGGGGGGMDAVLLDD-----
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  YGGFPPEAN-YLFLGDYVDRGKOSLETICLLLAYKIKYPENFFLLRGNHECASINRIYGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ICRAHOVVEDGYEFFADROLVTIFSAPNYCGEFDNAGAMMSVDETLMCSF-QILKPAERK 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLTDGEPLDKTEWQQIFDIMWSDP-QATMGCVPNTLRGAGVWFGPDVTDNFLQRHRLSY 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----AIFLSQ-----PNLLELEAPIK----ICGDIHGQYSDLLRLFEYGGFPP
                                                                                       ----KQVQL----SESEIRQLCTVSREIFLSQPNLLELEAPIKICGDIHGQYSDLLRLFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boukharov, Andrey A.
Barbazuk, Brad
                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                 12.4%;
                                                                                                                                                                                                                                                               63;
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                                                                                                                                                                                                                                                           Score 427; DB 4;
Pred. No. 1.4e-26;
3; Mismatches 136
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                                                                                                                                                                                                                                                                                                      Length 322;
                                                                                                                                                                          --IIRR-----LLEVRTARPG-
                                                                                                                                                                                                                                                             Indels
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RESULT 40
US-10-425-115-293336; Ay
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_17920C.1.
US-10-424-599-194787
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US-10-424-599-194787
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APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
FULE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 194787
LENGTH: 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 194787, Application US/10424599 Publication No. US20040031072A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 12.4%; Score 427; DB 4; Length 329; Local Similarity 31.1%; Pred. No. 1.4e-26;
                                                                                                                                                                                                                                                                                                                                                                    119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158 DIHGKIDDILYVIHKNGIPSSSNPYVFNGDFVDRGKRGIEVILILISIYIAPPNAVFINR
                                                                                                                                                                                                                                                                                                                     277 STSLDLIKSIDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMGCVPNTLRGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232 IREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGFS-DSTSLDLIKSIDRGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 DVHGQYSDLLRLFEYGGLPPRSN-YLFLGDYVDRGKQSLETICLLLAYKIKYPNNFFLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 INRLLEV-RGRPGKQVQ-----LSEA--EIKQLCLVSRDIFLRQPNLLELEAPIKICG
                                                                                                                                                                                                                   VWEGEDVTDNELQRHRLSYVIRSHECKENGHEEMHDNKIITIFSASNYYAIGSNKGAYIR 396
                                                                                                                                                 LNNQLMPHFVQYISAASQTKRLSFKQRMGIVBSSALKELAVRMR 440
                                                                                                                                                                                            YTFGADRVTEFLQKHDLDLICKAHQVVEDGYEFFANRQLVTIFSAPNYCGEFDNAGAMMT
                                                                                                                                                                                                                                                                                 LHNLNQIKGLPR----
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                                                                                                           VDETLVCSF-QILKPVENKKPSKF----GFGSTTTVKQSTTKAK 319
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  Application US/10425115
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: Lavord, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 29336
LENGTH: 322
TYPE: PRT
ORGANISH: Zea mays
PEATURE:
OTHER INFORMATION: Clone ID: MRT4577_30603C.1.pep
US-10-425-115-293336
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Search completed: January 20, Job time: 118 secs
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                                                                                                                        416 KRLSFKQRM 424
                                                                                                                                                                  255 ICRAHQVVEDGYEFFADRQLVTIFSAPNYCGEFDNAGAMMSVDETLMCSF-QILKFAERK 313
                                                                                                                                                                                                       356 VIRSHECKPNGHEFWHDNKIITIFSASNYYAIGSNKGAYIRLNNQLMPHFVQYISAASQT 415
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                   2006, 20:03:36
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
         Score
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1: /cgm2_6/ptodatea/1/pubpaa/USO6_NEW_PUB.pep:*

2: /cgm2_6/ptodatea/1/pubpaa/USO6_NEW_PUB.pep:*

3: /cgm2_6/ptodatea/1/pubpaa/USO7_NEW_PUB.pep:*

4: /cgm2_6/ptodatea/1/pubpaa/USO7_NEW_PUB.pep:*

5: /cgm2_6/ptodatea/1/pubpaa/USO9_NEW_PUB.pep:*

6: /cgm2_6/ptodatea/1/pubpaa/USO1_NEW_PUB.pep:*

6: /cgm2_6/ptodatea/1/pubpaa/USO1_NEW_PUB.pep:*

8: /cgm2_6/ptodatea/1/pubpaa/USO1_NEW_PUB.pep:*
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Gapop 10.0 , Gapext 0.5
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Sequence 38, Appl
Sequence 184, Appl
Sequence 37, Appl
Sequence 34, Appl
Sequence 24, Appl
Sequence 903, Appl
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Sequence 813, App
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Sequence 817, App
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Sequence 7, Appli
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Publication No. US20050250144Al
GENERAL INFORMATION:
APPLICANT: Toshio Ota
APPLICANT: Tetsuo Nishikawa
APPLICANT: Tetsuo Nishikawa
APPLICANT: Kaoru Otsuka
APPLICANT: Kaoru Otsuka
APPLICANT: Shiruko Ishii
APPLICANT: Shiruko Ishii
APPLICANT: Tomoyasu Sugiyama
APPLICANT: Ai wakamatsu
APPLICANT: Keichi Nagai
APPLICANT: Keichi Nagai
APPLICANT: Tetsuji Otsuki
APPLICANT: Tetsuji Otsuki
APPLICANT: Shin-Ichi Funahashi
APPLICANT: Shin-Ichi Funahashi
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US-11-109-156-38
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95	95	95.5	96.5	97	97	97	97	97	97.5	97.5	98	98	98	98	98	98	98.5	98.5	99
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252	225	2897	1145	4384	1184	814	216	216	613	467	5935	5464	5415	5406	5335	1538	749	746	276
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US-10-118-590-22	US-10-118-590-30	US-10-499-715-2	US-10-793-626-1432	US-10-821-234-1120	US-11-115-639-50	US-10-878-556A-161	US-10-118-590-6	US-10-118-590-2	US-10-131-826A-190	US-11-156-084-115	US-10-995-561-776	US-10-995-561-775	US-10-995-561-779	US-10-995-561-774	US-10-995-561-777	US-10-995-561-772	US-11-074-176-54	US-11-074-176-314	US-10-467-657-2502
Sequence 22, Appl	Sequence 30, Appl	Sequence 2, Appli	Sequence 1432, Ap		Sequence 50, Appl	Sequence 161, App	Sequence 6, Appli	Sequence 2, Appli	Sequence 190, App	Sequence 115, App	Sequence 776, App	Sequence 775, App	77	Sequence 774, App	Sequence 777, App	Sequence 772, App	Sequence 54, Appl	Sequence 314, App	Sequence 2502, Ap

## ALIGNMENTS

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US-11-109-156-38	ORGANISM: Homo sapiens	TYPE: PRT	LENGTH: 319	SEQ ID NO 38	SOFTWARE: Patentin Ver. 2.0	NUMBER OF SEQ ID NOS: 43	PRIOR FILING DATE: 2000-06-09	PRIOR APPLICATION NUMBER: JF 2000-241899	PRIOR FILING DATE: 2000-05-02	PRIOR APPLICATION NUMBER: JP 2000-183767	PRIOR FILING DATE: 2000-01-11	PRIOR APPLICATION NUMBER: JF 2000-118776	PRIOR FILING DATE: 1999-07-29	PRIOR APPLICATION NUMBER: JP 11-248036	PRIOR FILING DATE: 2000-02-17	PRIOR APPLICATION NUMBER: US 60/183,322	PRIOR FILING DATE: 1999-10-18	PRIOR APPLICATION NUMBER: US 60/159,590	PRIOR FILING DATE: 2000-07-28	PRIOR APPLICATION NUMBER: PCT/JP00/05061	PRIOR FILING DATE: 2002-01-29	PRIOR APPLICATION NUMBER: US/10/060,065	CURRENT FILING DATE: 2005-04-19	CURRENT APPLICATION NUMBER: US/11/109,156	FILE REFERENCE: 06501-099002	TITLE OF INVENTION: PHOSPHATASE	TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN	APPLICANT: Jun-Ichi Nezu	APPLICANT: Chiaki Senoo	

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RESULT 2
US-10-878-556A-184
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CURRENT FILING DATE: 2004-06-28
NUMBER OF SEQ ID NOS: 199
SOFTWARE: PatentIn version 3.1
SEQ ID NO 184
LENGTH: 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 184, Application US/10878556A Publication No. US20050266399A1 GENERAL INFORMATION:
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Best Local :
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Best Local Similarity
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ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: sw hum/pplg_human
DATABASE ENTRY DATE: 1994-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hoffmann La-Roche Inc.
TITLE OF INVENTION: HCV regulated protein expression
FILE REFERENCE: 21762
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                         RGAGVWFGPDVTDNFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKG 392
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RGVSFTFGAEVVAKFLHKHDLDLICRAHQVVEDGYEFFAKRQLVTLFSAPNYCGEFDNAG
                                                                                  SPDLQSMBQIRRIMR---
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Pred. No. 2.7e-24;
58; Mismatches 126;
                                                                               ----PTDVPDQGLLCDLLWSDPDKDVLGWGEND-
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US-11-109-156-37
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PRIOR FILING DATE: 1999-10-18
PRIOR PPLICATION NUMBER: US 60/183,322
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: UP 11-248036
PRIOR FILING DATE: 1999-07-29
PRIOR PPLICATION NUMBER: UP 2000-118776
PRIOR PILING DATE: 2000-01-11
                                                                                                                                                                                                                                                                                                                                                   Query Match 11.8%; Score 405.5; DB 7 Best Local Similarity 32.4%; Pred. No. 2.8e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. SEQ ID NO 37
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APPLICANT: Toshio C
APPLICANT: Takao I
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                                                                                                                                                                                                                                                                                                                                   Matches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
TITLE OF INVENTION: PHOSPHATASE
FILE REFERENCE: 06501-099002
CURRENT APPLICATION NUMBER: US/11/109,156
CURRENT FILING DATE: 2005-04-19
FRIOR APPLICATION NUMBER: US/10/66,065
PRIOR PILING DATE: 2002-01-29
PRIOR PILING DATE: 2000-07-28
PRIOR PILING DATE: 2000-07-28
PRIOR PILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-07-28
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TYPE: PRT
ORGANISM: Homo sapiens
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FILING DATE: 2000-05-02
  177
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                                                                                                                                                                                     155 VCGDLHGKLDDLLVVLHKNGLPSSSNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVF
                                                                                                                                                                                                                                                                                        102 KWHIDLLIDVFRKKRGWR-----LHPKYV-ALILREAAKSLKQLPWISPVSTAVSQQVT 154
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SPDLOSMEQIRRIMR---
                                    S-DSTSLDLIKSIDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDP-QATMGCVPNTL 332
                                                                                                                    LNRGNHBDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGF 274
                                                                                                                                                                                                                                                 KLNIDSIIQRLLEVRGSKPGKNVQLQENEIRGLCLKSREIFLSQ-----PILLELEAPLK
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                                                                               LLRGNHECASINRIYGFYDECKRRY--NIKLWKTFTD-CFNCLPIAAIVDEKIFCCHGGL
                                                                                                                                                               ICGDIHGQYYDLLRLFEYGGFPPESN-YLFLGDYVDRGKQSLETICLLLAYKIKYPENFF
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Jun-Ichi Nezu
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Tetsuji Otsuki
Shin-Ichi Funahashi
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Jun-Ichi Yamamoto
Shizuko Ishii
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Tetsuo Nishikawa
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PTDVPDQGLLCDLLWSDPDKDVLGWGEND-
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US-11-109-156-34
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; ORGANISM: Homo sapiens
US-11-109-156-34
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CURRENT FILING DATE: 2005-04-19
PRIOR APPLICATION NUMBER: US/10/060,065
PRIOR FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: PCT/JP00/05061
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/159,590
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-18
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Best Local Similarity
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APPLICANT:
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PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: JP 2000-118776
PRIOR FILING DATE: 2000-01-11
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TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
TITLE OF INVENTION: PHOSPHATASE
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                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE:
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APPLICATION NUMBER: JP 2000-241899
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   153
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                                                                    Toshio Ota
Takao Isogai
Tetsuo Nishikawa
CRHLTEYFTFKQBCKIKY---SERVYDACMDAFDCLPLAALMNQQFLCVHGGLSPEINTL 209
                                    DSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGFS-DSTSL 280
                                                                                                                                               KPRVDILKAHLMKE--GRLEESVALRIITEGASILRQEKNLLDIDA----PVTVCGDIHG
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Chiaki Senoo
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Tetsuji Otsuki
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ilarity 31.1%;
Conservative 5
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Pred. No. 6.8e-23;
8; Mismatches 119;
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US-11-109-156-24
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US-11-109-156-24
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SOFTWARE: PATENTIN VER. 2.0
SEQ ID NO 24
LENGTH: 309
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Best Local Similarity
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PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/159,590
PRIOR FILING DATE: 1999-10-18
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CURRENT FILING DATE: 2005-04-19
PRIOR APPLICATION NUMBER: US/10/060,065
PRIOR FILING DATE: 2002-01-29
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PRIOR FILING DATE: 2000-06-09
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TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
TITLE OF INVENTION: PHOSPHATASE
FILE REFERENCE: 06501-099002
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FILING DATE: 2000-01-11
APPLICATION NUMBER: JP 2000-183767
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FILING DATE: 2000-02-17
APPLICATION NUMBER: JP 11-248036
FILING DATE: 1999-07-29
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                                        179 SNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFFNAVFLNRGNHEDSVMNARYGFIREVESK 238
                                                                                                                      119 RLHPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLLVVLHKNGLPSS
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78 TN-YLFMGDYVDRGYYSVETVTLLVALKVRYRERITILRGNHESRQITQVYGFYDECLRK 136
                                                                                 22 QLSESQVKSLCEKAKEILTKESNVQEVRC----PVTVCGDVHGQFHDLMELFRIGGKSPD
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Takao Isogai
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Tetsuji Otsuki
Shin-Ichi Funahashi
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Jun-Ichi Yamamoto
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                                                                                                                                                                   11.0%; Score 379; DB 7;
31.1%; Pred. No. 2.9e-22;
tive 62; Mismatches 112
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                                                                                                                                                                                                            Length 309;
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                                                                                                                                           Query Match 11.0%; Score 379; DB 7; Length 309; Best Local Similarity 31.1%; Pred. No. 2.9e-22; Matches 91; Conservative 62; Mismatches 112; Indels
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SEQ ID NO 39
LENGTH: 309
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Publication No.
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APPLICANT:
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APPLICANT: Takao Isogai
APPLICANT: Tetsuo Nishikawa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLIATION NUMBER: PCT/JP00/05061
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/159,590
PRIOR FILING DATE: 1999-10-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/11/109,156
CURRENT FILING DATE: 2005-04-19
PRIOR APPLICATION NUMBER: US/10/060,065
PRIOR FILING DATE: 2002-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN TITLE OF INVENTION: PHOSPHATASE FILE REFERENCE: 06501-099002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 43
                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: JP 2000-118776
PRIOR FILING DATE: 2000-01-11
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FILING DATE: 2000-02-17
APPLICATION NUMBER: JP 11-248036
                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: JP 2000-183767 FILING DATE: 2000-05-02
                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: JP 2000-241899
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                                      179
                                                                                                       119 RLHPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLLVVLHKNGLPSS
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Keiichi Nagai
Tetsuji Otsuki
Shin-Ichi Funahashi
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SNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNARYGFIREVESK
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                                                                     QLSESQVKSLCEKAKEILTKESNVQEVRC----PVTVCGDVHGQFHDLMELFRIGGKSPD
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No. US20050250144A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tomoyasu Sugiyama
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Shizuko Ishii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chiaki Senoo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kaoru Otsuka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Koji Hayashi
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                                                                                                                                                                                                                                                                                                                                           141
                  GFDIIDMTAGGQIN----SDQRRNLGSVAKVLQHAASNKLFEGENEHLSSMNNYLSETYQ
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PILE REPERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 903
LENGTH: 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-10-821-234-903
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Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
302 G-EPLDKTEWQQIFDIMWSDPQATMGCVPNTLRGAG---VWFGPD----VTDNFL----Q 349
                                                                                                                                                                                                                                                                                                                                                                     986 IKSKVDQVQDIVTGNPTVIKMVVSFN-----RGARGQNTLRQLLAPVVKBIIDDKSLIIN 1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                926 QLFYLLQTNPLYLAKLIFQMPQNKSTKFMDTVIFTLYNYASNQREBYLLLKLFKTALEBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           808 DYKTLVGSENPPLTVIRKFVYLLDQSDLDFQEELEVARLREEVVTKIRANQQLEKDLNLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  762 SVVKIQSWFRMATARKSYLSR------LQYFRDHNN-EIVK-----IQSLLRANKARD 807
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                                                                                                                                                                                                                          TNPVEVYKÄWVNQLETQTG----EASKLPYDVTTEQALTYPEVKNKLEASIENLRRVTDK 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIKIGLLV-KNRI-TLEDVISHSKKLNKKKGGEMEILNNTDNQGIKSLSKERRKTLETYQ 925
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                                                                                                                                                                                                                                                                                          ----LYLAFPNAVFLNRGNHEDSVMNARYGFIREVESKYPRNHKRILAFIDEVYR---- 255
                                                                                                                                                                                                                                                                                                                                                                                                                                             -----SSNPYV-----FNGDFVDRGKRGLEVLLLLLS-------
                                                                           VLNSIISSLDLLPYGLRYIAKVLKNSIHEKFPDATEDELLKIVGNLLYYRYMNPAIVAPD
                                                                                                                                               -----WLPLGSVLNSRVL--IVHGGFSDSTSLDLIKSIDRGKYVSILRPPLT--D 301
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19.8%; Pred. No. 0.33;
1tive 122; Mismatches 274; Indels 28
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QY 454DPKDSGYISISHWCKVMENVTKLGLPWRLLRDKLAPGTDSQKVNYNRTLDL 504    :-   :    :-   :    :-   :-   :-   :	QY 434 ELAVRMRDHR 453 : : : : :       : : : : : : :       : :   : : : : : : : : : : : : : : : : : : : :	OY 377TIFSASNYYAIGSNKGAYIRLANNQLMPHFVQYISAASQTKRLSFKQRMGIVESSALK 433	OY 331 TLRGAGVWFGPDVTDNFLQRHRLSYVIRSHECKPNGHBFMHDNKII 376	OY 273 GFSDSTSLDLIKSJDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMGCVPN 330           :   :   :   :   :   :           :	Query Match 3.2%; Score 111; DB 6; Length 548; Best Local Similarity 18.6%; Pred. No. 0.4; Matches 86; Conservative 67; Mismatches 175; Indels 134; Gaps 19;	TYPE: PRT  CRGANISM: Homo sapiens  US-10-995-561-810	SEQ ID NOS: FastSEQ for 810	DETECTION AND USES THEREOF 59 MBER: US/10/995,561 2004-11-24	; GENERAL INFORMATION: ; APPLICANT: CARGILL, Michele et al. ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH ; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE. METHODS OF	RESULT 8 US-10-995-561-810 ; Sequence 810, Application US/10995561 ; Publication No. US20050272054A1	1528 KGVLLDID	638 NTLVVBHD 645	Qy 609	Qy 567 SKAEMLEKCRMMDINGDGKVDINEFIEAFRISDIHRKEQQDE 608   :	QY 508 DVILEAEADGMSVMDALYANKASLVAIFNIIDADNSGEITLDEFETAIDLLV-AHMPGAY 566	Qy 449 EF-RKYDPKDSGYISISHWCKVMENVTKLGLPWRLLRDKLAPGTDSQKVNYNRTLDLLDT 507	QY 405 -FVQYISAASQTKRLSFKQRMGIVESSALKELAVRMRDHRDELED 448 :::   :   :   :   :   :   :   :   :   :	Qy 350 RHRLSYVIRSHECK-PNGHEFMHDNKIITIFSASNYVAIGSNKGAYIRLNNQLMPH- 404
RESULT 10 US-10-995-561-812 ; Sequence 812, Application US/10995561	Qy 614 STGRPSVAKTATDPVTLLADKISKNTLVVEHDIDPTDCE 652	QY 565 AYSKAEMLEKCRMMDLNGDGKVDLNB	QY 505 LDTDVILEARADGMSVMDALYANKASLVAIFNIIDADNSGEITLDEFETAIDLLVAHMPG 564	Qy 454DPKDSGYISISHWCKVMENVTKLGLPWRLLRDKLAPGTDSQKVNYNRTLDL 504   :-	QY 434 ELAVRMRDHR	QY 377TIFSASNYYAIGSNKGAYIRLNNQLMPHFVQYISAASQTKRLSFKQRMGIVESSALK 433	Qy 331 TLRGAGVWFGPDVTDNFLQRHRLSYVIRSHECKPNGHEFMHDNKII 376	Qy 273 GFSDSTSLDLIKSIDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMGCVPN 330           :   :   :   :   :	Query Match 3.2%; Score 111; DB 6; Length 567; Best Local Similarity 18.6%; Pred. No. 0.42; Matches 86; Conservative 67; Mismatches 175; Indels 134; Gaps 19;	; LENCTH: 567 ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-995-561-813		CURRENT APPLICATION NUMBER: US/10/995,561	; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: DETECTION AND USES THEREOF ; FILE REFERENCE: CL001559	; Publication No. US20050272054A1 ; GENERAL INFORMATION: AICHele et al. ; APPLICANT: CARGILL, Michele et al.	RESULT 9 US-10-995-561-813 : Sequence 813. Application US/10995561	Qy 614 STGRPSYAKTATDPVTILADKISKNTLVVEHDIDPTDCE 652	Qy 565 AYSKAEMLEKCRMMDLNGDGKVDLNEFLEAFRLSDLHRKEQQDENIRRR 613	Qy 505 LDTDVILBARADGMSVMDALYANKASLVAIFNIIDADNSGBITLDBFBTAIDLLVAHMPG 564       :   :   :   :   :   :   :   :   :

Gaps

104

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APPLICANT: Klaenhammer, Todd R.
APPLICANT: Russell, William M.
APPLICANT: Altermann, Eric
APPLICANT: Altermann, Eric
APPLICANT: McAuliffe, Olivia
APPLICANT: McAuliffe, Olivia
APPLICANT: McAuliffe, Olivia
APPLICANT: McIdeic Acid Sequences Encoding
TITLE OF INVENTION: Stress-Related Proteins and Uses The
FILE REFERENCE: 5051-694
CURRENT APPLICATION NUMBER: US/11/074,176
CURRENT APPLICATION NUMBER: 60/551,161
PRIOR APPLICATION MUMBER: 60/551,161
PRIOR FILING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 381
                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
US-11-074-176-158
; Sequence 158, Application US/11074176
; Publication No. US20050250135A1
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SOFTWARE: FASTSEQ for Windows Version 4.0; SEQ ID NO 812
LENGTH: 599
TYPE: PRT
ORGANISM: Homo sapiens
US-10-995-561-812
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APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE,
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
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            SOFTWARE:
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          PastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ST---GRPSVAKTATDPVTLLADKISKNTLVVEHDIDPTDCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKVDLGCTSEENSVKQND-----VDMLNVFDFEKAGNSEPNELKNESEVTIQQERQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSEMNIKQASNCVTYDAKEKIAPLPLEGHDSTWDEIKDDALQHSSPRAMCQYSLKPPSTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---SSGALYGRRPRSTFPNSHRFQLVISK---APSGDLLDKHSELFSNKQLPFTPRTLKT
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          4.0
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                                                                                             US-11-202-516-10

Sequence 10, Application US/11202516

Publication No. US20060008465A1

GENERAL INFORMATION:

APPLICANT: Steinaa, Lucilla

APPLICANT: Mouritsen, Soren

APPLICANT: Balum, Iben

APPLICANT: Haaning, Jesper

APPLICANT: Haaning, Jesper

APPLICANT: Heach, Dana

APPLICANT: Karlsson, Gunilla

APPLICANT: Rasmussen, Peter
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LENGTH: 709
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APPLICANT: Nielsen, Klaus
APPLICANT: Karlsson, Gunilla
APPLICANT: Rasmussen, Peter
TITLE OF INVENTION: Novel Methods for Therapeutic
FILE REFERENCE: 4614-0107PUS2
CURRENT PEPLICATION NUMBER: US/11/202,516
CURRENT FILING DATE: 2005-08-11
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TYPE: PRT
ORGANISM: Lactobacillus acidophilus
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Local Similarity 17.4%; Pred. No. 1;
hes 113; Conservative 97; Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      581 NG----FRLSDLHR 602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       474 VNKLIGSAPGYVGYGEGGQLTEKVRHQPYSLILFDEIEKANPQVFNALLQIMDDGRLTDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 RGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNARYGFIREVESKYPRNHKRILAFIDEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 NISPVSTAVSQQV-----TVCGDLHGKLDDL-LVVLHKNGLPSSSNPYVFNGDFVDRGK
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; PRIOR APPLICATION NUMBER: US 09/806,703
; PRIOR FILLING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: PCT/DK99/00525
; PRIOR APPLICATION NUMBER: PCT/DK99/00525
; PRIOR APPLICATION NUMBER: DK 1998 01261
; PRIOR FILLING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: US 60/105,011
; PRIOR FILLING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PATENTIN VERSION 3.0
; SEQ ID NO 10
; ELNCTH: 694
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-202-516-10
                                                                                                                                                                     RESULT 13
US-11-202-516-8
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                                                                 Sequence 8, Application US/11202516
Publication No. US20060008465A1
GENERAL INFORMATION:
APPLICANT: Steinaa, Lucilla
APPLICANT: Mouriteen, Soren
APPLICANT: Gautam, Anand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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                  APPLICANT:
APPLICANT:
APPLICANT:
   APPLICANT:
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            Haaning, ver
Haaning, ver
Thach, Dana
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                                                                                                                                                                                                                                                                                                                                 TKLGLPWRLLR------DKLAPGTDSQKVN------YNRTLDLLDTDVILEAEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                    TOKVIOHIHSYTKVTRI-----YNVIGTLKGA-----LEPD--RYVILGGHRDAW 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRLNNQLMPHFVQYISAASQTKRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGVQRGNVLNLNGA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSVLNSRVLIVHGGFSDSTSLDLIKSIDRGKYVSILRPPLTDGEPLDKTEWQQ------
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                                                                                                                                                                                                                                                                                                    ----RLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELQSPDEGFE---
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                                                 Gautam, Anand
Dalum, Iben
 Nielsen, Klaus
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Pred. No. 1.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GDPLTPGYPANEHAYRHELTNAVG
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                                                                 RESULT 14
US-10-793-626-2964
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Sequence 2964, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
                                                                                                                                                                 516 DGMSVMDA 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 GGVQRGNVLNLNGA-----
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                                                                                                                                 -GKSLYDS
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APPLICANT: Karlsson, Gunilia
APPLICANT: Rasmussen, Peter
TITLE OF INVENTION: Novel Methods for Therapeutic Vaccination
FILE REFERENCE: 4614-01079US2
CURRENT APPLICATION NUMBER: US/11/202,516
CURRENT FILING DATE: 2005-08-11
PRIOR APPLICATION NUMBER: US 09/806,703
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: PCT/DX99/00525
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 60/105,011
PRIOR PILING DATE: 1998-10-05
PRIOR PILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 33
SOPTWARE: PatentIn version 3.0
SEQ ID NOS
LENGTH: 752
TYPE: PRT
ORGANISM: Mus musculus
US-11-202-516-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.1%; Score 107.5; Best Local Similarity 19.9%; Pred. No. 1.2; Matches 109; Conservative 72; Mismatches
                                                                                                                                                                                                                                             341 TQKVKMHIHSYTKVTRI------YNVIGTLKGA-----LEPD--RYVILGGHRDAW
                                                                                                                                                                                                                                                                                                      359 SHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRLNNQLMPHFVQYISAASQTKRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215 MYKNAQLAGAKGMIL----YSDP---ADY-FVPAVKS-YPDG------WNLPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 LLLSLYLAFPNAVFLNRGNHEDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRW-LPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 VSTAVSQQVTVCGDL----HGKLDDLLVVLHKNGLPSSSNPYVFNGDFVDRGKRGLEVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 EL----SHYDVLLSY-----PNKTHPNYISIINEDGNEIFKTSLSEQPPPGYENISDVVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 EFLHELKAENIKKFLYNFTR-TPHLAGTQNNFELAKQI-----HDQWKEFGLDLV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 EYASEQDQAELYKFFNDLIKHMPQAAGRKNQYQGSAHVSVLDDKDDLVEEFG-DIVNAKI 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSVLNSRVLIVHGGFSDSTSLDLIKSIDRGKYVSILRPPLTDGEPLDKTEWQQ-----
                                                                                                                     VFGGIDPQSGAAVVHEIVRSFGTLKKKGRRPRRTILFASWDAEEFGLLGSTEWAEEHS--
                                                                                                                                                                                                                                                                                                                                                                  LPSIPVHPIGYDDAQKLLEHMGGPAPPDSSWKGGLKVPYNVGPGFAGNF------
----RLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELQSPDEGFE---
                                                                                                                                                                              SF-----KORMGIVESSALKELAVRMRDHRDELEDEFRKYDPKDSGYISISHWCKVMENV
                                                                                                                                                                                                                                                                                                                                                                                                                               -----FGPDVTDNFLQRHRLSYVIR 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELPIRKNHIDLLIDVFRKKRGNRLHPKYVALILREAAK----SLKQLP-----NIS---P
                                                         DKLAPGTDSQKVN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 752;
                                                         -YNRTLDLLDTDVILEAEA
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US-10-793-626-2964
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CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2964
LENGTH: 5024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 149;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (5024)
OTHER INFORMATION: variable amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3761 IATASNNALALNKVMGKLEQFINHADSIENS-----DNYRQADDDKIIAYDDALEHG 3812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3725 EA-----KVHANQTIDQL---THLNSLQQQT------AKESVKNATKLEE 3760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3665 LPNYTEASEDKKEKVDQTVSHAQAIIDKINGSNVSLDQVRQALEQLTQASENLDGDQRVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3991 KAQFTHANDEIMNTNSIAQLSRIVNQAFDLNDAMKSLRDELNNQAFF--VQASSNYINSD 4048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3813 QDIQKSNATQNEAKQALQQLINAETSL--NGFERLNHARPRALEYIKSLEKINNAQKSAL 3870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3605 NDEIKHMNYLNNAQKQSIKDMISHAALRTEVKQLLQQAKTLDEAMKSLEDKTQVVITDTT 366
                                                                                                                                                                                                                                                                                                             467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 NDLIKHM------PQAAGRKNQYQGSAHVSVLDDKDDLVBEFGDIVNAKIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LP-----IRKNHIDLLID----VFRKKRGNRLHPKYVALILREAAKSLKQLPNISPVS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAVSQQVTVCGDLHGK--LDDLLVVLHKNGLPSSSNPYVFNGDFVDRGKRGLEVLLLLLS
                            -IYDTKNALNGEQRLATEKSKDLKLIKGLKDLNKAQLED-----VTNKVNSANTLTELS
                                                                                                                                     DLRDTLESNSTSVPNSVNYINADKNLQIEFDEALQQASATSSKTSENPATIEEVLGLSQA
                                                                                                                                                                                            --- DALYANKASLVAIFNIIDADNSGEITLDEF---ETAIDLLVAHMPGAYSKAEMLEKC
                                                                                                                                                                                                                                                   AKAIQYVQSLSYI-----NDAQRHIAESNIHNSDDLSSLANTLSKASDLDNAMK 4152
                                                                                                                                                                                                                                                                                                       CKVMENVTKLGLPWRLLRDKLAPGTDSQK----VNYNRTLDLLDTDVILEAEADGMSVM-
                                                                                                                                                                                                                                                                                                                                                              E-----DLKQQFDHALSNARKVLAKENGKNLDEIQIEGLKQVIEDTKDALNGIQRLSKAK 4103
                                                                                                                                                                                                                                                                                                                                                                                                                     SQTKRLSFKQRMGIVESSALKELAVRMRDHRDELEDEFRKY---DPKD--SGYISISH-W 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AINNARDALNKTQGQNLDFNAIDTFKDDIFKTKDALNGIERLTAAKSKAEKLIDSLKFIN 3990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RPPLTDGEPLDK-----TEWQQIFDIM------WSDPQATMGCVP------
                                                                                 RMMD----LNGDGKV--DLNEFLEAFR-LSDLHRKEQQDENIRRRSTGRPSVAKTAT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----NTLRGAGVWFGPDVT---DNFLQRHRLSYVIRSHBCKPNGHBFMHDNKII- 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative 105; Mismatches 274;
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Pred. No. 30
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TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells

FILE REFERENCE: 1581.0800001

CURRENT APPLICATION NUMBER: US/11/062,471A

CURRENT FILING DATE: 2005-02-22

PRIOR APPLICATION NUMBER: 09/831,050

PRIOR FILING DATE: 1999-11-05

PRIOR FILING DATE: 1999-11-05

PRIOR APPLICATION NUMBER: PCT/GB99/03699

PRIOR APPLICATION NUMBER: B8 9824282.9

PRIOR APPLICATION NUMBER: 05 9824282.9

PRIOR FILING DATE: 1998-11-05

NUMBER: OF SEQ ID NOS: 11

SOPTWARE: Patentin Ver. 2.1

SEQ ID NO 4

LENGTH: 1070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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Best Local Similarity 18.7%;
Matches 116; Conservative 98
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APPLICANT: SHONE, Clifford Charles
APPLICANT: SUTTON, John Mark
APPLICANT: HALLIS, Bassam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/11062471A Publication No. US20050255093A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             643 IILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               478 LIVAQWLSTVNTQFYTIKEGMYKALNYQA-QALEEIIKYRYNIYSEKEKSNINIDFNDIN 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 IFIQKWY-----RRHQARREMQRRCNWQIFQNLE-----YASEQDQAELYKFFND--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --LIKHMPQAAGRKNQYQGSAHVSVLDDK--DDLVEBFGDIVNAKIELPIRKNHIDLLID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----NKLY--LIGSAEYEKSKVNKYLKTIMPFDLSIYTNDTILIEMFNKYNSEILNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VFRKKRGNRLHPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKL------
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A-----GNKNSYIKLKKDSPVGBILTRSKYNQNSKYINYRDLYIGE-----KFIIRRK 929
                                                 ASNYYAIGSNKGAYIRLNNQLMPHFVQYISAASQTKRLSFKQRMGIVESSALKELAVRMR
                                                                                                                                                                                                                                                                       GGFSDSTSL-DLIKSIDRGKYVSILRPPLTDGEPLDKTE--WQQIFDIMWSDPQATMGCV
                                                                                                                                                                                                                                                                                                                                                                                        -----RYGPIREVESKYPRNHKRILAFIDEVYRW--LPLGSVLNSRVLIVH 271
                                                                                                                                                                                                                                                                                                                                                                                                                                            LD-----FSV8FWIRIPKYKNDGIQNYIHNBYTIINCMKNNSGWKISIRGNRIIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VDRGKRGLEVLLLLSLYLAFP---NAVFLNRGNHEDSVMNA---------
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                                                                                                                                                                  PNTLRGAGVWFGPDVTDNFLQRHRLSYVIRSHECKPNGHEFMHD-----NKIITIFS
                                                                                                                                                                                                                         GKLESNTDIKDIREVIANGEIIFKL----DGD-IDRTQFIWMKYF8I-------
                                                                                                                                                                                                                                                                                                                                    TLIDINGKTKSVFFEYN-IREDISEY-----INRWFFVTITNNLNNAKIYIN
                                                                                                           - FNTELSQSNIBER---YKIQSYS-----EYLKDFWGNPLMYNKBYYMFN
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Pred. No. 3.4;
98; Mismatches
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US/11/062,471A-7
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CURRENT FILING DATE: 2005-02-22
PRIOR APPLICATION NUMBER: 09/831,050
PRIOR FILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: PCT/GB99/03699
PRIOR APPLICATION NUMBER: PCT/GB99/03699
PRIOR FILING DATE: 1999-11-05
PRIOR PRIOR FILING DATE: 1998-11-05
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PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1998-11-05
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SILMAN, Nigel
TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
FILE REFERENCE: 1581.0800001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SHONE, Clifford Charles
APPLICANT: SUTTON, John Mark
APPLICANT: HALLIS, Bassam
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
OTHER INFORMATION: Construct comprising a mitochondrial leader sequence from
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                                                                                                                                                                                                                                                                                                                                                                                       617
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PNTLRGAGVWFGPDVTDNFLQRHRLSYVIRSHECKPNGHEFMHD------
                                                                                                                                            TLIDINGKTKSVFFEYN-IREDISEY-----INRWFFVTITNNLNNAKIYIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IFIQKWY-----RRHQARREMORRCNWQIFQNLB-----YASEQDQAELYKFFND--
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                                                                                                                                                                                                                          LD-----FSVSFWIRIPKYKNDGIQNYIHNBYTIINCMKNNSGWKISIRGNRIIW 777
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                                                                                                  GGFSDSTSL-DLIKSIDRGKYVSILRPPLTDGEPLDKTE--WQQIPDIMWSDPQATMGCV 328
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Pred. No. 3.6;
98; Mismatches
                                                            ----LPSSSNP-----YVFNGDF 188
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US-10-055-877-140
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US-10-118-590-18
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US-10-118-590-18
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Publication No. US20050277761A1
GENERAL INFORMATION:
APPLICANT: KENNETH RHODES, MARIA BETTY, HUAI-PING
TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
LENGTH: 270
                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                              Sequence 140, A Publication No.
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Best Local
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                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                           APPLICANT: DeCristofaro, Marc
APPLICANT: Padigaru, Muralidi
APPLICANT: Miller, Charles
APPLICANT: Tcherney, Velizar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: MNI-070
CURRENT APPLICATION NUMBER: US/10/118,590
CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US/09/298,731
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 47
                         APPLICANT:
                                                                                    APPLICANT:
                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59;
                  Ballinger, Robert
Gerlach, Valerie
Spytek, Kimberly
Ratelli, Luca
Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                                                                       REEAPREHVESFFQKMDRNKDGVVTIBEFIESC-----
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                                                                                                                                                                              Padigaru, Muralidhara
Miller, Charles
                                                                                                                       Anderson, David
                                                                                                                                            Zhong,
                                                                                                                                                                                                                                                              Application US/10055877
o. US20050288241A1
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Pred. No. 0.59;
25; Mismatches
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; ORGANISM: Mus musculus
US-10-055-877-140
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CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: 60/262,892
PRIOR FILING DATE: 2001-01-19
PRIOR PPLICATION NUMBER: 60/263,598
PRIOR PPLICATION NUMBER: 60/263,598
PRIOR PPLICATION NUMBER: 60/263,799
PRIOR PPLICATION NUMBER: 60/264,117
PRIOR APPLICATION NUMBER: 60/264,117
PRIOR APPLICATION NUMBER: 60/264,117
PRIOR APPLICATION NUMBER: 60/264,139
PRIOR APPLICATION NUMBER: 60/264,139
PRIOR APPLICATION NUMBER: 60/264,139
PRIOR APPLICATION NUMBER: 60/264,478
PRIOR APPLICATION NUMBER: 60/264,478
PRIOR APPLICATION NUMBER: 60/264,478
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Best Local Similarity
Matches 107; Conserv
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SEQ ID NO 140
LENGTH: 1765
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REFERENCE: 21402-251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2001-01-26
APPLICATION NUMBER: 60/263,351
FILING DATE: 2001-01-30
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                                     234
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                               EVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVH-GGFSDSTSLDLIKSIDRGKYV
                                                                                                                                            LHVAAK-----GKSGLTPLHVAAH
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SVHLAAQEGH-----VDMV-----SLLLSRNANVNLSNKSGLTPLHLAAQEDRVNVA
                                                                     YDNQKVALLLLD-QGASPHAAAKNGYTPLHIAAKKNQMDIATSLLEYGADANAVTRQGIA
                                                                                                                                                                                                                    AATTSGYTPLHLAAREGHED--
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                                                                                                          ---- EVILLLISLYLAFPNAVFLN------RGNHEDSVMN-ARYGF----
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Taupier Jr., Raymond
Pena, Carol
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Shimkets, Richard
Gusev, Vladimir
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                                                                                                                                                                                                                                                                                                                                                           3.0%; Score 103; DB 6; Length 1765; ilarity 21.1%; Pred. No. 9.4; Conservative 54; Mismatches 177; Indels 16
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Sequence 268, Application US/11124368A

Publication No. US20050287559A1

GENERAL INFORMATION:
APPLICANT: Michele Cargill
APPLICANT: May Luke
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Vascular Diseases, Methods of Detection and
FILE REFERENCE: CL001524
CURRENT APPLICATION NUMBER: US/11/124,368A
CURRENT PILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,845
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US-10-821-234-1535
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SEQ ID NO 1535
LENGTH: 149
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APPLICANT: Stache-Crair
APPLICANT: Andarmani, (
APPLICANT: Tang, Y. Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.0%; Score 102; DB Best Local Similarity 28.1%; Pred. No. 0.3; Matches 39; Conservative 20; Mismatches
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CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
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TITLE OF INVENTION: Methods for Diagnosis
PRIOR FILING DATE: 2004-05-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        737 AKVNAKTKNGYTALHQAAQQGHTHI-INVLLQNNASPNELTVNGNTALAIARRLG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                   109 VMTNLGEKLTDEEVDEMIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 MINEVDADGNGTIDFPEFLT---MMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRH 108
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                                                                                    RESULT 22
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US-11-124-368A-269
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; ORGANISM: Homo sapiens
US-11-124-368A-268
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 3.0%; Score 102; DB 7; Length 149; Best Local Similarity 28.1%; Pred. No. 0.3; Matches 39; Conservative 20; Mismatches 58; Indels
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SEQ ID NO 268
LENGTH: 149
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CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,845
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/625,936
PRIOR FILING DATE: 2004-11-09
NUMBER OF SEQ ID NOS: 21112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Genetic Polymorphisms Associated with TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof FILE REFERENCE: CL001524
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PRIOR FILING DATE: 2004-11-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 149
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                           534 IFNIIDADNSGEITLDEFETAIDLLVAHMPGAYSKAEMLEKCRMMDLNGDGKVDLNEFLE 593
                                                                                                                                                     109 VMTNLGEKLTDEEVDEMIR 127
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                                                                                                                                                                                                                                                                                                                                      1 MADQL---TEEQIABFKEAFSLFDKD-----GDGTITTKELGTVMRSLGQNPTEAELQD 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Mismatches 58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 46, Application US/11065943 Publication No. US20050250131A1
                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                           Best Local
                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: JESTIN, JEAN-LUC
APPLICANT: VICHIER-GUERRE, SOPHIE
APPLICANT: PERRIS, STEPHANE
TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
TITLE OF INVENTION: VARIABTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVIT
TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
FILE REFERENCE: 26642GUSOXCIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/11/065,943
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: US 10/787,219
PRIOR FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 106
SOFTWARE: PatentIn version 3.3
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APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT APPLICATION NUMBER: US/10/821,234
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PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 148
TYPE: PRT
ORGANISM: Homo sapiens
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601 HRKEQQDENIR 611
                                                                                                     542 NSGEITLDEFETAIDLLVAHMPGAYSKAEMLEKCRMMDLNGDGKVDLNEFLEAF-RLSDL 600
                                                                                                                                                                                                         491 TDSQKVNYNRTLDLLDTDVILEAEADGM-----SVMDALYAN--KASLVAIFNIIDAD 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 VMTNLGEKLTDEEVDEMIR 149
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                                                                                                                                                                                                                                                                37;
                                                    59 GNGTIDPPEFLT---MMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEK 115
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                                                                                                                                                    5 TEEQIABPKEAPSLPDKD-----GDGTITTKELGTVMRSLGQNPTEAELQDMINEVDAD
                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                         2.9%; Score 101.5; D
28.2%; Pred. No. 0.32;
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US-11-108-172-1095
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US-10-118-590-16
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US-10-118-590-16
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Best Local Simi
Matches 56;
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CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US/99/298,731
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
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Publication No. US20050277761A1
GENERAL INFORMATION:
APPLICANT: KENNETH RHODES, MARIA BETTY, HUAI-PING LING, AND FRANK AN
TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT: Clapper, Jonathan D.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Panger, Garry R.
APPLICANT: Vedvick Thomas S.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C15
CURRENT APPLICATION NUMBER: US/11/108,172
CURRENT FILING DATE: 2005-04-15
PRIOR APPLICATION NUMBER: US 10/025,380
PRIOR FILING DATE: 2001-12-19
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 GFKNECPSGIVNEENFKQIYSQFFPQGDSS--NYATFLFNAFDTNHDGSVSFEDFVAGLS
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                                                                                                                                                                                                                                                                                                                        Stolk, John A. Wang, Tongtong
                                                                                                                                                                                                                                                                                                                                                                                      Secrist, Heather
Benson, Darin R.
                                                                                                                                                                                                                                                                                  Jiang, Yuqiu
Smith, Carole L.
                                                                                                                                                                                                                                                                                                                                                                   Meagher, Madeleine Joy
                                                                                                                                                                                                                                             King, Gordon E.
Wang, Aijun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.9%; Score 101; DB ilarity 24.9%; Pred. No. 0.79 Conservative 27; Mismatches
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Pred. No. 0.79;
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US-11-108-172-1095
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PRIOR PILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: US 09/504,629
PRIOR FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: US 09/480,321
PRIOR FILING DATE: 2000-01-10
PRIOR APPLICATION NUMBER: US 09/476,296
PRIOR APPLICATION 1099-12-30
PRIOR PILING DATE: 1999-12-30
Remaining Prior Application data removed - Se
NUMBER OF SEQ ID NOS: 1130
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SEQ ID NO 1095
LENGTH: 1548
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Best Local Similarity 20.7%;
Matches 111; Conservative 69
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FILING DATE: 2001-08-03
APPLICATION NUMBER: US 09/833,263
FILING DATE: 2001-04-10
APPLICATION NUMBER: US 09/649,811
FILING DATE: 2000-08-28
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                                            518 MSVMDALYANKASLVAIFNIIDAD-----NSGEITLDEFE----TAIDLLVA 560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 VLSDVVSVBTPGCPABFLNIRIPPGDPVFDPDQRGDVVLPFQRSRW----DPBTGRSPSN 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198 VLLLLLSLYLAFPNAVFLN-------RGNHEDSVMNARYGFIREVESKYPRNH
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GPLFSAIVLDQ-----FVRLRDGDRYWFENTRNGLFSKKEIEDIRNTTLRDVLVA
                                                                                                                                                                                                                         IVESSALKELAVRMRDHRDELED-----EFRKYDPKDSGYISISHWCKVMENVTKLGLP- 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                         QNPL-----LMWAAPDPATG--QNGPRGLYAFGAERGNREPFLQALGLLWFRYHN 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRDLA--NQVTGWLD-GSAIY-----GSSHSWS-DALRSFSGGQLASGPDPAFPRDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KRILAPIDEVYRWLPLGSVLNSRVLIVHGGPSDSTSLDLIKSIDRGKYVSILRP--PLTD
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                                                                                       YSQALLAFGLDIPRNW----SDLNPNVDPQVLEATAALYNQDLSQLELLLGGLLESHGDP
                                                                                                                                                                              LNSTQEVNELLLGMASQISELEDNIVVEDLRDYWPGPGKFSRTDYVASSIQRGRDMGLPS
                                                                                                                                                                                                                                                                                                                   IITIF--SASNYYAIGSNKGAYIRLNNQLMPHFVQYIS---AASQTKRLS----FKQRMG
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                                                                                                                                    ----YNRTLDLLDTDV--ILEAEADG
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Pred. No. 12;
65; Mismatches
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RESULT 26 US-10-467-657-2502

Sequence 2502, Application US/10467657 Publication No. US20050260581A1 GENERAL INFORMATION:

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FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SegWin99, version 1.04
SEQ ID NO 2502
LENGTH: 276
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US-11-074-176-314
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                                                                                                                                                                                                                                                                                                                                                               Sequence 314, Application US/11074176 Publication No. US20050250135A1
PRIOR APPLICATION NUMBER: 60/551,161
PRIOR FILING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 314
LENGTH: 746
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Best Local Similarity
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                                                                                                                    APPLICANT: Russell, William M.
APPLICANT: Altermann, Bric
APPLICANT: McAuliffe, Olivia
APPLICANT: McAuliffe, Olivia
APPLICANT: McAuliffe, Olivia
APPLICANT: McAuliffe, Olivia
APPLICANT: Peril, Andrea Azcarate
TITLE OF INVENTION: Nucleic Acid Sequences Encoding
TITLE OF INVENTION: Stress-Related Proteins and Uss
FILE REFERENCE: 5051-694
CURRENT APPLICATION NUMBER: US/11/074,176
CURRENT FILING DATE: 2005-03-07
                                                                                                                                                                                                                                                                                                APPLICANT: Klaenhammer, Todd R. APPLICANT: Russell, William M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: CHIRON SPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 RGNHEDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGFSD 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --W-----KMYGNKPAAW 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGNHDLYLLAVGCG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --FKAPDRQNLDHTIIFGHWSSLGYTNADNVISLDTGALW-------GGQLTAVN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDIQGCFDELTALLGKIGFNHGTDTLWLTGDIVNRGPKSLET----LQFCIRHENSVQIV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----YIRLINNQLMPHFVQYISAASQTKRLSFKQRMGIVESSALKELAVRMRDHRDELE 447
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Pred. No. 1.3;
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APPLICANT: Klaenhammer, Todd R.
APPLICANT: Russell, William M.
APPLICANT: Altermann, Eric
APPLICANT: Altermann, Eric
APPLICANT: McAuliffe, Olivia
APPLICANT: Peril, Andrea Azcarate
TITIZ OF INVENTION: Nucleic Acid Sequences Encoc
TITIZ OF INVENTION: Stress-Related Proteins and
FILE REFERENCE: 5051-694
CURRENT APPLICATION NUMBER: US/11/074,176
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: 60/551,161
PRIOR APPLICATION WIMBER: 60/551,161
PRIOR FILING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 54
LENGTH: 749
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; ORGANISM: Lactobacillus acidophilus
US-11-074-176-314
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Publication No. US20050250135A1
GENERAL INFORMATION:
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Best Local Similarity
TYPE: PRT
ORGANISM: Lactobacillus acidophilus
-11-074-176-54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --QGSAHVSVLD----DKDDLVEBFGD----IVNAKIBLP-----IRKNHIDLLI-
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Pred. No. 5.
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                                                                                                                                                                                                                           Encoding
ns and Uses Therefore
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Sequence 772, Application US/1095561

Publication No. US20050272054A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CL001559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT APPLICATION NUMBER: US/10/995,561

NUMBER OF SEQ ID NOS: 85702

SOCTUARE: FastSEQ for Windows Version 4.0

SEQ ID NO 772

LENGTH: 1538
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                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-772
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US-10-995-561-772
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                                                                                          Matches 154;
                                                                                                                                   Query Match
                                                                                                            Local Similarity
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                                           AIFIQKWYRRHQARREMORR------CNWQIF--QNLEYASEQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HGEQMVANTIRDEGLVPKDFMDKEHIEKLLEHFNYNTSEEL
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    ALLEQKW----HVVSSKMEERKSKLEEALNLATEFONSLOEFINWLTLAEOSLNIASPPSL
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                                                                                   2.8%; Score 98; DB ilarity 18.9%; Pred. No. 19; Conservative 103; Mismatches
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-777
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US-10-995-561-777
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                                                                               Sequence 777, Application US/10995561

Publication No. US20050272054A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS (
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE REFERENCE: CL001559

FILE REFERENCE: CL001559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT PILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: PAStSEQ for Windows Version 4.0
                                                                 LENGTH: 5335
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US-10-95-561-774

US-10-95-561-774

; Sequence 774, Application US/10995561

; Publication No. US20050272054A1

; Publication No. US20050272054A1

; Publication No. US20050272054A1

; GENERAL INFORMATION:
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    GENERAL INFORMATION:
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    GENERAL INFORMATION:
    DETECTION AND USES THEREOF

; FILE REFERENCE: CL001559
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2.8%; Score 98; DB 6; Length 5335;
Best Local Similarity 18.9%; Pred. No. 1.2e+02;
Matches 154; Conservative 103; Mismatches 265; Indels 2
  CURRENT APPLICATION NUMBER: US/10/995,561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILNTVLSQIBEHKVFANEVNAHRDQIIELDQTGNQLKFLSQKQDVVLIKNLLVSVQSRWE 4480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----DQABLYKFF-NDLIKHMPQ-----AAGRKNQYQGSAH------VSV----
                                                                                                                                                                                                                                                                                                                      VAALHPNKDAYRPTTDADKIEDEVTROVAQCKCA 5083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VWILALER-----QRKLN-----DALDRIEELKEFANFDFDVWRKKYMRWMNHKKSRVM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLSVSKQSRLEQALKQAEVFRDTVHMLLEWLSEA----EQTLRFRGALFDDTEA-LQSLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLHGKLDDLLVVLHKNGLPSSSNPYVFNGDFVDRGKR------GLE 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVVQRSIERGRSLDDARKRAKQFHEAWKKLIDWLEDAESHLDSELEISNDPDKIKLQLSK 4540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -WRLLRDKLAPGTDSQKVNYNRTLDLLDTDVILEAEAD-----GMSVMDALYANKASLV 532
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RESULT 32
US-10-995-561-779
; Sequence 779, A
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; ORGANISM: Homo
US-10-995-561-774
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Matches 154
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NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 774
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Similarity 18.9%;
54; Conservative 10
                                                                                                                                                                                                                      DFFRRIDKDQDGKITRQ8F---IDGILASKFP--TTKLEMTAVADIFDRDGDGYIDYY8F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----DOABLYKFF-NDLIKHMPQ-----AAGRKNOYQGSAH------VSV-----
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                                                                                                                                                                                                                                                    AIFNIIDADNSGEITLDEFETAID-LLVAHMPGAYSKAEMLEKCRMMDLNGDGKVDLNEF 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LMPHFVQYISAASQT-------KRLSFKQRMGIVESSALKELAVRMRDHRD 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----ESKYPRNHKRILAFIDEVY---RWLPLGSVLNSRVLIVHGGFSDSTSLDLIKSI 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLHGKLDDLLVVLHKNGLPSSSNPYVFNGDFVDRGKR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KVVQRSIERGRSLDDARKRAKQFHEAWKKLIDWLEDAESHLDSELBISNDPDKIKLQLSK 461:
                                                                                                                                                                                                                                                                                                                         VWLLALER-----QRKLN-----DALDRLEBLKEFANFDFDVWRKKYMRWMNHKKSRVM
                                                                                                                                                                                                                                                                                                                                                                    -WRLLRDKLAPGTDSQKVNYNRTLDLLDTDVILEABAD-----GMSVMDALYANKASLV 532
                                                                                                                                                                                                                                                                                                                                                                                                                       RVTKTYKRKNIEPTHAPFIEKSRSGGRKSLSQPTPPPMPILSQSEAKNPRINQLSARWQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DRGKYVSILRPPLIDGEPLDKTEWQQIFDIMWSDPQATMG-----CVPNTLRGAGVWFG 340
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     Application US/10995561
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Pred. No. 1.2e+02;
)3; Mismatches 265
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US-10-995-561-779
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 779
LENGTH: 5415
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DFFRRIDKDQDGKITRQEF---IDGILASKFP--TTKLEMTAVADIFDRDGDGYIDYYEF
                                                                                                                                                                                        RVTKTYKRKNIEPTHAPFIEKŚRŚGGRKSLSQPTPPPMPILSQSEAKNPRINQLSARWQQ 503
                                                                                                                                                                                                                        LLEELLAWIQWAETTLIQRDQBPIPQNIDRVKAL-----IAEHQTFMEEMTRKQPDVD
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                                                                                                                                          -WRLLRDKLAPGTDSQKVNYNRTLDLLDTDVILEAEAD-----GMSVMDALYANKASLV 532
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                                                                                             --DALDRLEELKEFANFDFDVWRKKYMRWMNHKKSRVM
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US-10-995-561-775
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US-10-995-561-775
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Sequence 775, Application US/2054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USSS THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION UMBER: US/10/995,561
CURRENT FILLING DATE: 2004-11-24
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 775
LENGTH: 5464
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Matches 154;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4573 KVVQRSIERGRSLDDARKRAKQFHEAWKKLIDWLEDAESHLDSELEISNDPDKIKLQLSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 ---FRKKRGNRLHPKYVALILRBAAKSLKQ---LPNISPVSTAVSQQV-----TVCG--- 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198 VLLLLLSLYLAFPNAV-----FLNRGNHEDSVMNAR-----YGFIREV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 DLHGKLDDLLVVLHKNGLPSSSNPYVFNGDFVDRGKR-------GLE 197
                                             445 BLBDEFRK--YDPKD8GYI--SISHWCKVMENVTKLGLP---------
                                                                                                                                          401 LMPHFVQYISAASQT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 -----DQAELYKFF-NDLIXHMPQ-----AAGRKNQYQGSAH------VSV-----
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RVTKTYKRKNIBPTHAPFIEKSRSGGRKSLSQPTPPPMPILSQSBAKNPRINQLSARWQQ
                                                                                                                                                                                          ----TITRARFEEVLTWAK-----QHQQRLETALSE--
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                                                                                          LIEELLAWIQWAETTLIQRDQEPIPQNIDRVKAL----IAEHQTFMEEMTRKQPDVD
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RESULT 34
US-10-995-561-776
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Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARCILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS
TITLE OF INVENTION: DETECTION AND USES THEREOP
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 776
LENGTH: 5935
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                                                                           PDVTDNFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRLNNQ 400
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                          -TIIRARFEEVLTWAK-----QHQQRLETALSE---
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; SEQ ID NO 115
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Medicago truncatula
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US-11-156-084-115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.8%; Score 97.5; DB 7; Best Local Similarity 18.5%; Pred. No. 3.5; Matches 81; Conservative 54; Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Monsanto Technology LLC
TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads
TITLE OF INVENTION: agronomically interesting phenotypes
FILE REFERENCE: (38-21)
CURRENT APPLICATION NUMBER: US/11/156,084
CURRENT FILING DATE: 2005-06-17
NUMBER OF SEQ ID NOS: 364
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-RLSYVIRSHECKPNGHE
                                                                                                EWQQIFDIMWSDPQATMGCVPNTLRGAGVWFGPDVTDNFLQRH-------
                                                                                                                                                   SILSKSNDIWNRQVVESATKIVTTFVSENGSLLSTFGMSNGTGTKIIQRDL------
                                                                                                                                                                                                                                                                                                                                                          -----GVREFEDLL------RTSVFKNINQREGELIDG-----SSLENSEPLF 295
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                                                  ----YTCKACNDRVLRGLHEW-
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                                                EQHIRGRGHRKRISSLKSKA 446
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RESULT 36 US-10-131-826A-190

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                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 69; Conserv
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 190
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PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
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CURRENT FILING DATE: 2002-04-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/059588
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APPLICATION NUMBER: 60/059184
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APPLICATION NUMBER: 60/
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406 -VQYISAASQTKRLSFKQRMGIVESSALKELAVRMRDHRDELEDEFRKYDPKDSGYISIS 464
                                                                 245 NFNDSVLESGHECYHPNMPDAFLTCETVIFAWAIGGEGFSYPPHVGLSLGTPLDPHYVLL
                                                                                                                                                                                          306 DKTEWQQIFDI-MWSDPQATMGCVPNTLRGAGVWFGPDVTDNFLQRHRLSYVIRSHECKP
                                                                                                         N-----GHEFMHDN---KIITIFSASNYYAIGSNKGAY----IRLNNQLMPHF---
                                                                                                                                                   DTTYWCQMFKIPVFQEKHHVIKVEPVIQRG-----HESLVHHILLY-----QCSN 244
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Wood, William
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Godowski, Paul J.
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                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                    2.8%; Score 97.5; DB 6;
21.4%; Pred. No. 5.3;
ative 38; Mismatches 103;
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                                                                                                                                                                                                                                                                              Length 613;
                                                                                                                                                                                                                                      Indels 113;
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SEQ ID NO 6 LENGTH: 216 TYPE: PRT

SOFTWARE: PatentIn Ver.

CURRENT APPLICATION NUMBER: US/10/118,590 CURRENT FILING DATE: 2002-04-08 PRIOR APPLICATION NUMBER: US/09/298,731 PRIOR FILING DATE: 1999-04-23 NUMBER OF SEQ ID NOS: 47

FILE REFERENCE: MNI-070

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US-10-118-590-6
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US-10-118-590-2
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Sequence 6, Application US/10118590
Publication No. US20050277781A1
GENERAL INFORMATION:
APPLICANT: KENNETH RHODES, MARIA BETTY, HUAI-PING LING, AND FRANK AND TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2
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Best Local &
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PRIOR APPLICATION NUMBER: US/09/298,731
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KENNETH RHODES, MARIA BETTY, HUAI-PING TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS FILE REFERENCE: MNI-070
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 216
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                                                                                                                                                                                     MMGKYTYPVLKEDTPRQHVDVFFQKMDKNKDGIVTLDEFLESC----
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CURRENT APPLICATION NUMBER: US/10/878,556A
CURRENT FILING DATE: 2004-06-28

NUMBER OF SEQ ID NOS: 199
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 161
LENGTH: 814
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: sw hum/if39 human
DATABASE ENTRY DATE: 1997-11-01
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US-10-878-556A-161
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Publication No. US20050266399A1
GENERAL INFORMATION:
APPLICANT: Hoffmann La-Roche Inc.
TITLE OF INVENTION: HCV regulated protein expression
FILE REFERENCE: 21762
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les 50; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      484 RDKLAPGTDSQKYNYNRTLDLLDTDVILEABADGMSVMDALYA----NKASLVA--IFN
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                                                                                                                                                                                   NGDF----VDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNARYGFIREVESKYP
                       DFRKY---
                                                                                                                                                                                                                            HRLSYVIRSHECKPNGHEFMHDNKIITIFS----ASNYYAIGSNKGAYIRLNNQLMPHF
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                                                           EFRKYDPKDSGYISISHWCKVMENVTKLGLPWRLLRDKLAPGTDSQKVNYN-----RTL 502
                                                                                                      CQLLWRPRPPTLLSQEQIKQIKKDLKKYSKIFEQKDRLSQSKASKELVERRR----TMME
                                                                                                                                         VQY-----ISAASQTKRLS-----FKQRMGIVESSALKELAVRMRDHRDELED
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                       -RKMAQELYMEQKNERLELRGGVDTDELDSNVDDWEEETI 799
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; TYPE: PRT
; ORGANISM: L. |
US-11-115-639-50
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APPLICANT: Murphy, Christopher
APPLICANT: Murphy, Christopher
APPLICANT: MacNeil, Ian
TITLE OF INVENTION: SCREENING ASSAYS FOR ANTIMICROBIAL
TITLE OF INVENTION: AGENTS
FILE REFERENCE: 50150/075003
CURRENT APPLICATION NUMBER: US/11/115,639
CURRENT FILING DATE: 2005-04-27
PRIOR APPLICATION NUMBER: 60/566,858
PRIOR FILING DATE: 2004-04-30
PRIOR FILING DATE: 2004-04-30
PRIOR PILING DATE: 2004-04-30
PRIOR PILING DATE: 2004-04-30
PRIOR SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
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US-11-115-639-50
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Publication No. US20050282242A1
GENERAL INFORMATION:
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Best Local
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                                        NVTKLGLPWRL-----LRDKLAPGTDSQKVNYNRTLDLLDTDVILBA-----B
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                                                                                                                                                                                                                                                                                                                               DNARSLLV-SRFFDPKRYDL-ASVGRYKINKKLHLKNRLFNQTLAETLVDPETGEIIASK 309
                                                                                                                                                                                                                                                                                                                                                                     LNSRVLIVHGGFSDSTSLDLIKSIDRGK-----YVSILRPPLTD------
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DMTTI-TPQQLINIRPVVASIKEFFGSSQLSQFMNQTNPLDELTYKRRLSALGPGGLTRB
                                                                                                                          -FKQRMGIVESSALKELA-VRMRDHRDELEDEFRKYDFKDSGYISISHWCKV-----ME 471
                                                                                                                                                                                                         ECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRLNNQLMPHFVQYISAASQTKRLS- 419
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88; Mismatches
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Search Job ti	망	8	В	Ş	Ф	Ş
Search completed: January 20, 2006, 20:04:22 Job time : 37 secs	607 ERIDYMDVSPKQVVSVATACIPFLENDDSNRALM 640	608 ENIRRETGRPSVAKTATDPVTLLADKISKNTLV 641	555 THRVTDKIDYLTADEEDNYVVAQANSKLDEQGTFTEEEVMARFRSENLAVEK 606	553 TAIDLLVAHMPGAYSKAEMLEKCRMMDLNGDGKVDLNEFLEAFRLSDLHRKEQQD 607	499 RAGYEVRDVHYSHYGRMCPIETPEGPNIGLENYLSSFAKVNKFGFIETPYRRVDPE 554	VAIFNIIDADNSG

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Result
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F;152-221/Domain: phosphopseterase core homology <PEC>
F;526-558/Domain: calmodulin repeat homology <EF1>
F;556-598/Domain: calmodulin repeat homology <EF1>
F;158,160,187/Binding site: iron (Asp, His, Asp) #status predicted
F;187,219,271,360/Binding site: zinc (Asp, Asn, His, His) #status predicted
F;190,220,384/Active site: Asp, His, Tyr #status predicted
F;191,333/Binding site: substrate phosphate (Arg) #status predicted
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Cell 69, 669-676, 1992
A;Title: Drosophila retinal degeneration C (rdgC) encodes a novel serine/threonine protone a:Reference number: A42287; MUID:92266398; PMID:1316807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphoprotein phosphatase (EC 3.1.3.16) rdgC - fruit fly (Drosophila melany N;Alternate names: retinal degeneration protein C C;Species: Drosophila melanogaster C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 12-Jul-2004 C;Accession: A42287; S27811 R;Steele, F.R.; Washburn, T.; Rieger, R.; O'Tousa, J.E.
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A;Gene: rdgC
A;Cross-references: FlyBase:FBgn0004366
A;Introns: 5/1; 47/3; 74/3; 116/3; 172/3; 240/3; 290/3; 312/3; 374/3; 510/3; 544/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Note: sequence extracted fr , NCBIN:103104, NCBIP:103001)
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A;Residues: 1-661 <STE>
A;Cross-references: UNIPROT:P40421; UNIPARC:UPI0000072EA; EMBL:M89628; NID:g158237; PII
A;Note: sequence extracted from NCBI backbone (NCBIN:103017, NCBIN:103023, NCBIN:103028)
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Best Local Similarity 100.0%; 1
Matches 661; Conservative 0;
181
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                                                                                               HPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLLVVLHKNGLPSSSN
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PYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNARYGFIREVESKYP 240
                                                           HPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLLVVLHKNGLPSSSN
                                                                                                                                                                                    QAAGRKNQYQGSAHVSVLDDKDDLVEEFGDIVNAKIELPIRKNHIDLLIDVFRKKRGNRL
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Pred. No. 1.5e-208;
0; Mismatches 0;
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C,Accession: T4239
R,Sherman, P.M.; Sun, H.; Macke, J.P.; Williams, J.; Smallwood, P.M.; Nathans, J. Proc. Natl. Acad. Sci. U.S.A. 94, 11639-11644, 1997
A,Title: Identification and characterization of a conserved family of protein serine/thm A;Reference number: Z22115; MUID:97471020; PMID:932663
A,Accession: T42239
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Rosidues: 1-707 <SHE>
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T42239
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               LDDLLVVLHKNGLPSSSNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHED
                                                   PQVAKMIEAF--KVNKVLHPKYVLMILHEARKIFKAMPSVSRISTSISNQVTICGDLHGK
                                                                                                          GGVENGRNS PLMSALSHYAKPSLMDSEGETVKKMLEDTS PTNVDIDRNYKGPTLSLPLDK
                                                                                                                                      KNQYQG--SAHVSVLDD--KDDLVEEFGDIVNAKIE-----
                                                                                                                                                                               IRAAIFIQKWYRRHQARREMQRRCWWQIFQNLEYASEQDQAELYKFFNDLIKHMPQAAGR 65
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                                                                                                                                                                 IKSAILIQKWYRRCEARLEARRRATWQIFTALEYAGEQDQLKLYDFFADVIRAMAEENGK 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         661
                                                                                                                                                                                                                      38.3%; Score 1317; DB 2;
ilarity 42.1%; Pred. No. 5.3e-75;
Conservative 116; Mismatches 200
                                                                                                                                                                                                                         200;
                                                                                                                                                                                                                                                Length 707;
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A;Introns: 91/1; 139/3; 353/3; 5
C;Superfamily: serine/threonine
C;Keywords: EF hand
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Best Local S
Matches 266
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266; Conserv
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R-LNNQLMPHFVQYISAASQTKRLS-FKQRMGIVESSALKELAVRMRDHRDELEDEFRKY
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TDYISQIAESIDFNKDGFIDLNELLEAFRLVD
                                                                                                                                                                                         DIEKSGKLPILKWSDCVBRITGLNLPWIALAPKVATLSBDGKYVMYKBDRRIAQVGGTHA
                                                                                                                                                                                                                                    DPKDSGYISISHWCKVMENVTKLGLPWRLLRDKLAP-GTDSQKVNYNRTLDLLDTDVILE
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                                        ----LEKCRMMDLNGDGKVDLNEFLEAFRLSD
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734072
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Decies: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 12-Jul-2004
C;Accession: T34072
R;Rohlfing, T:; Wohldmann, P:
submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid F23H11.
A;Reference number: Z21470
A;Accession: T34072
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residuss: 1-722 <ROH>
A;Fesiduss: 1-722 <ROH>
A;Genetics:
C;Genetics:
A;Genetics: 91/1; 139/3; 353/3; 579/1; 674/3
C;Superfamily: serine/threonine protein phosphatase with BF-hands; calmodulin repeat hom

AMABENGKGGVENGRNSPLMSALSHYAKPSLMDSEGETVKKMLEDTSPTNVDIDRNYKGP VCGDLHGKLDDLLVVLHKNGLPSSSNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVF NAIRAAIFIQKWYRRHQARREMQRRCNWQIFQNLEYASEQDQAE-----LYKFFNDLIK ICGDLHGKFDDLCIILYKNGYPSVDNPYIFNGDFVDRGGQSIEVLCVLFALVIVDPMSIY TLSLPLDKPQVAKMIEAF--KVNKVLHPKYVLMILHEARKIFKAMPSVSRISTSISNQVT ---LPIRKNHIDLLIDVFRKKRGNRLHPKYVALILREAAKSLKQLPNISPVSTAVSQQVT HMPQAAGRKNQYQG--SAHVSVLDD--KDDLVEEFGDIVNAKIE-----STIKSAILIQKWYRRCEARLEARRRATWQIFTALEYAGEQDQLKVRVWITLYDFFADVIR 37.9%; llarity 41.6%; Conservative 11: 117; Score 1305; DB 2; Pred. No. 3.1e-74; 7; Mismatches 201; 201; Length Indels 56; Gaps 149 214 154 209 267 327 97 13

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hypothetical protein - Trypanosoma cruzi
(;Species: Trypanosoma cruzi
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999
C;Accession: T14614
R; Andersson, B.; Aslund, L.; Pettersson, U.
submitted to the EMBL Data Library, March 1998
A;Description: 93.4 kb of complete sequence from ch
A;Reference number: Z18159
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                    AYSKAEM-----LEKCRMMDLNGDGKVDLNEFLEAFRLSD 599
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                        SQTK------RLSFKQRMGIVESSA--
                                                                                                                    SYVIRSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAY-IRLNNQLMPHFVQYISAA
                                                                                                                                                                ---PMPD---YSQPEEDE I FQDLLWSDPVEDLQGWRESPRGAGVVFGADVTQEFLQNNGL
                                                                                                                                                                                                            LRPPLTDGEPLDKTEWQQIF-DIMWSDPQATMGCVPNTLRGAGVWFGPDVTDNFLQRHRL
                                                                                                                                                                                                                                                          TKYDRN----VFRLVQRCFCALPLATIIGKKVFVVHGGLPRRKGVNIEDISRIQRFRQI--
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                                                                      ELVIRSHEECLRGYEEHHDGKLLTVFSASNYDGPETNFGSFAVFVGDNPEPSFHTYQVAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.2%; Score 593.5; DB 2; 33.0%; Pred. No. 1.5e-29; tive 73; Mismatches 204;
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A; Oross-references: UNIPARC:UPI0000172827; GB:X77237
A; Note: authors translated the codon AAG for residue 50 as Gln, and GTA for residue C; Superfamily: protein phosphates 5; phosphoesterase core homology; phosphoprotein C; Keywords: iron; metalloprotein; nucleus; phosphoric monoester hydrolase; zinc R; 28-61/Domain: tetratricopeptide repeat homology <TT1>
F; 62-95/Domain: tetratricopeptide repeat homology <TT2>
F; 96-129/Domain: phosphoprotein phosphatese homology <TF3>
F; 204-468/Domain: phosphoprotein phosphatese homology <PPP>
F; 236-305/Domain: phosphoprotein phosphatese homology <PPP>
F; 236-305/Domain: phosphoprotein phosphatese homology <PPC>
F; 242, 244, 271/Binding site: zinc (Asp, His, His, His, His) #status predicted
F; 271, 303, 352, 427/Binding site: xinc (Asp, Asn, His, His, His) #status predicted
F; 274, 304, 451/Active site: Asp, His, Tyr #status predicted
F; 277, 400/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Becker, W.; Kentrup, H.; Klumpp, S.; Schultz, J.E.; Joost, H.G. J. Biol. Chem. 269, 22586-22592, 1994
A;Title: Molecular cloning of a protein serine/threonine phosphatase A;Reference number: A55346; MUID:94357899; PMID:8077208
A;Accession: A55346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphoprotein phosphatase (EC 3.1.3.16) PPT [validated] - rat W.Alternate names: serine/threonine phosphatase PP5 C.Species: Rattus norvegicus (Norway rat) C.Jate: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 28-Apr-2003 C.Jacession: A55346
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A; Residues: 1-499 <BE
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Best Local (
346 NFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRL-NNQLMPH 404
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                                                                                                                                                                312 IYGFEGEVKAKYT---AQMYELFSEVFEWLFLAQCINGKVLIMHGGLFSEDGVTLDDIRK 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                138 ECSKIVKQKAFERAIAGDEHRRSVVDSLDIESMTIEDEYSGPKLEDGKVTITFMKD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 FIQKWYRRHQARREMORRCNWQIFQNLBYASEQDQABLYKFFNDLIKHMPQAAGRKNQYQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 16.5%; Score 569; DB 1; Length 499; Similarity 33.7%; Pred. No. 3.3e-28; and 10; Indels 43; Conservative 73; Mismatches 140; Indels
                                                                                                                                                                                                                                                        RYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGF--SDSTSLDLIKS
                                                                                                                                                                                                                                                                                                      VVILHKNGLPSSSNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNA
                                                                                                                                                                                                                                                                                                                                                                                             LIDVFRKKRGNRLHPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLL
                                                                                                                  IDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMGCVPNTLRGAGVWFGPDVTD
                                                                                                                                                                                                                                                                                                                                                    LMQWYKDQK--KLHRKCAYQILVQVKEVLCKLSTLVETTLKETEKITVCGDTHGQFYDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FQPLWLNDWIQSA---CHHLTQQQRANHRSQY----VAKAFNKEQVSYNEFCSVIRAIDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --DLLDTDVILEABADGMSVMDALYANKASLVAIFNIIDADNSGEITLDEFETAIDLLVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YFAKLDRTRKGSVWKIEWVEAMRNVLNLDLPWFFLRGYLVADDENTRVWYSHFLVKFHNF 582
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                                                                        -dago-
                                                                      -DSGPM-----CDLLWSDPQPQNGRSVSK-RGVSCQFGPDVTK
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A;Description: catalyzes the hydrolytic dephosphorylation of protein-phosphoserine [valia,Note: may play a role in the regulation of RNA synthesis and mitosis C;Superfamily: protein phosphosphates 5; phosphosphoric monoester hydrolase; zinc C;Keywords: iron; metalloprotein; nucleus; phosphoric monoester hydrolase; zinc F;28-61/Domain: tetratricopeptide repeat homology <TT1> F;62-95/Domain: tetratricopeptide repeat homology <TT3> F;96-112/Domain: tetratricopeptide repeat homology <TT3> F;204-467/Domain: phosphorotein phosphatase homology <PP> F;236-305/Domain: phosphosterase core homology <PBC> F;236-305/Domain: phosphosterase core homology <PBC> F;242,244,271/Binding site: iron (Asp, Han, His, His) #status predicted F;271,303,352,426/Binding site: zinc (Asp, Asn, His, His) #status predicted F;274,304,450/Active site: Asp, His, Tyr #status predicted F;275,399/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Xu, X.L.; Lagercrantz, J.; Zickert, P.; Bajalica-Lagercrantz, Blochem. Blophys. Res. Commun. 218, 514-517, 1996
A;Title: Chromosomal localization and 5' sequence of the human A;Reference number: PC4136; MUID:96144708; PMID:8561788
A;Accession: PC4136
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A;Cross-references: GDB:136857
A;Map position: 19q13.3-19q13.3
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R;Chen, M.X.; McPartlin, A.B.; Brown, L.; Chen, Y.H.; Barker, H.M.; Cohen, P.T.W.
EMBO J. 13, 4278-4290, 1904
A;Title: A novel human protein serine/threonine phosphatase, which possesses four tetrat
A;Reference number: S52570; MUID:95009929; PMID:7925273
A;Accession: S52570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-37 < XUX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P53041; UNIPARC:UPI0000172826; EMBL:S73586; EMBL:X89416
A;Experimental source: teratocarcinoma cell line NTERA-2
R;Xu, X.L.; Lagercrantz, J.; Zickert, P.; Bajalica-Lagercrantz, S.; Zetterberg, A.
Biochem. Biophys. Res. Commun. 218, 514-517, 1996
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N;Alternate names: serine/threonine phosphatase PP5
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Best Local Similarity
Matches 144; Conserv
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RYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGFSDST-SLDLIKSI 286
                                                    NIFELNGLPSETNPYIFNGDFVDRGSFSVEVILTLFGFKLLYPDHFHLLRGNHETDNMNQ
                                                                                                              VVLHKNGLPSSSNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNA
                                                                                                                                                                                                                         LIDVFRKKRGNRLHPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLL 167
                                                                                                                                                                                                                                                                                                                                                                                               YIKGYYRRAASNMALGK----FR----AALRD-----YETVVKVKPHDKDAKKKYQ
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                                                                                                                                                                        LMQWYKDQK--KLHRKCAYQILVQVKEVLSKLSTLVETTLKBTEKITVCGDTHGQFYDLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                       ----GSAHV-SVLDDKD----DLVEEFG--DIVNAKIELPIRKNHIDL
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A;Note: Y3986B.ff
C;Superfamily: protein phosphatase 5; phosphoesterase core homology; phosphoprotein C;Superfamily: protein phosphatase; phosphoric monoester hydrolase; zinc C;Keywords: iron; metalloprotein; nucleus; phosphoric monoester hydrolase; zinc F;29-61/Domain: tetratricopeptide repeat homology <TT1>
F;62-95/Domain: tetratricopeptide repeat homology <TT3>
F;65-129/Domain: tetratricopeptide repeat homology <TT3>
F;203-497/Domain: phosphoprotein phosphatase homology <PEC>
F;231-304/Domain: phosphoesterase core homology <PEC>
F;235-304/Domain: phosphoesterase core homology <PEC>
F;241,243,270/Binding site: iron (Asp, His, Asp) #status predicted
F;273,303,480/Acctive site: Asp, His, Tyr #status predicted
F;273,480/Acctive site: Asp, His, Tyr #status predicted
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R.Wilson, R., Ainscough, R., Anderson, K.; Baynes, C.; Berks, M.; Bonfield, J.; Burton, raser, A.; Fulton, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier, M.; Johns B.; O'Callaghan, M.; Parsons, J.; Percy, C.; Rifken, L.; Roopra, A.; Saunders, D. Nature 368, 32-38, 1994

A;Authors: Shownkeen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonnhammer, E.; S tock, L.; Wilkinson-Sproat, J.; Wohldman, P.

A;Title: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.

A;Reference number: S43531; MUID:94150718; PMID:7906398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphoprotein phosphatase (EC 3.1.3.16) Y39B6B.ff [similarity] - Caenorhabditis elegans N/Alternate names: serine/threonine phosphatase PP5 homolog C;Species: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 3
A; Introns: 42/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPARC:UPI0000083436; EMBL:AL132896; NID:g6434440; PIDN:CAB60937.1; A;Experimental source: clone Y39B6B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-526 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                144 RROKFBAAISTDHDKKTVAETLDINAMAIEDSYD--GPRLEDKITKEFVLQLIKTFKNQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138;
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SETNPYLFNGDFVDRGSFSVET1FTM1GFKLLYPNHFFMSRGNHESDVMNKMYGFEGEVK
                                                                                 SSSNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNARYGFIREVE 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENAIRAAI --- FIQKWYRRHQARREMQR-RCNWQIFQNLEYASEQDQAELYKF--FNDLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRL-NNQLMPHF 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ERNR-----QPP--DSGPM------CDLLWSDPQPQNG-RSISKRGVSCQFGPDVTKA 412
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                                                                                                                                                                            --KLHKKYAFKMLLEFYNYVKSLPTMVEITVPTGKKFTICGDVHGQFYDLCNIFEINGYP
                                                                                                                                                                                                                                                     GNRLHPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLLVVLHKNGLP
                                                                                                                                                                                                                                                                                                                                                                                                                             KHMPQAAGRKNQYQGSAHVSVLDDKDDLVEBFGDIVNAKIBLPIRKNHIDLLIDVFRKKR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNAI--AIDPSYVKGFYRRATANMALGRFKKALTDYQAVVKVCPNDKDARAKFDECSKIV 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.2%; Score 558; DB 1; Length 526; 31.6%; Pred. No. 1.7e-27; tive 79; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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RESULT 8
E84858
phosphoprotein phosphatase (EC 3.1.3.16) At2g42810 [similarity] - Arabidopsis thaliana phosphoprotein phosphatase (EC 3.1.3.16) At2g42810 [similarity] - Arabidopsis thaliana (c;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: O2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 28-Apr-2003
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 28-Apr-2003
C;Accession: E84858
C;Accession: E84858
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, M.; Koo, H.; Moffat, M.; Koo, H.; WanAken, S.B.; Pager, C.M.; Venter, M.; Koo, H.; Moffat, M.; Koo, H.; Moffat, M.; Mo
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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: B49858

A;Status: preliminary
A;Accession: B49858
A;Status: preliminary
A;Residues: 1-533 <STO>
A;Cross-references: UNIPARC:UPI000044D6A; GB:AE002093; NID:94512673; PIDN:AAD21727.1; C;Genetics: At2942810
A;Map position: 2
C;Superfamily: protein phosphatase 5; phosphoesterase core homology; phosphoprotein phocy;Keywords: phosphoric monoester hydrolase
RESULT 9
T46576
Thosphoprotein phosphatase (EC 3.1.3.16) ppt-1 [similarity]
phosphoprotein phosphatase PP5 homolog
N;Alternate names: serine/threonine phosphatase PP5 homolog
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Best Local !
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                                                                                                                                                                                                                                                            GSNKGAYIRLN-NQLMPHFVQY
                                                                                                                                                                                                                                                                                                                      GPSK-RGVGLSEGGDVTKRFLQDNNLDLLVRSHEVKDEGYEVEHDGKLITVFSAFNYCDQ
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                                                                                                                                                                                                                                                                                                                                                                                  VPNTLRGAGVWFGPDVTDNFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNYYAI 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VHGG-FS-DSTSLDLIKSIDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITVCGDVHGQFYDLLNIFELNGLPSEENPYLFNGDFVDRGSFSVEIILTLFAFKCMCPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARIEGEEVTLDFVKTMMEDFKNQK--TLHKRYAYQIVLQTRQILLALPSLVDISVPHGKH
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                                                                                                                                                                                                         MGNKGAFIRFEAPDMKPNIVTF
                                                                                                                                                                                                                                                                                                                                                                                                                                            VHGGLFSVDGVKLSDIRAIDR----FCEPP-----EEGLMCBLLWSDPQPLPGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IYLARGNHESKSMNKIYGFEGEVRSKLSEK-----FVDLFAEVFCYLPLAHVINGKVFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 557.5; DB 2; ; Pred. No. 1.9e-27; 55; Mismatches 109;
                                                                                                                                                                                                                                                               408
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                                            Neurospora
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L.; Tallon, L
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      phosphoprotein phosphatase (BC 3.1.3.16) SPBC3F6.01c N;Alternate names: serine/threonine phosphatase PP5 h C;Species: Schizopaccharomyces pombe C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #t C;Accession: T40391 R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Churcher submitted to the EMBL Data Library, February 1998
                                                                                                                                                                                                                               RESULT 10
T40391
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A; Gene: ppt-1

A; Map position: V

C; Superfamily: protein phosphatase 5; phosphoesterase core homology; phoc; Superfamily: protein phosphatase 5; phosphoric monoester hydrolater 1; 100 perfamily: protein; nucleus; phosphoric monoester hydrolater 1; 100 perfamily: metalloprotein; nucleus; phosphoric monoester hydrolater; 100 perfamily: tetratricopeptide repeat homology <TT1>
F; 42-75/Domain: tetratricopeptide repeat homology <TT3>
F; 183-448/Domain: phosphorotein phosphatase homology <PPP>
F; 215-284/Domain: phosphoesterase core homology <PPC>
F; 221, 223, 250/Binding site: iron (Asp, His, Asp) #status predicted F; 250, 283, 331, 408/Binding site: zinc (Asp, Asp, His, His) #status predicted F; 253, 283, 432/Active site: Asp, His, Tyr #status predicted F; 254, 381/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Neurospora crassa
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2)
C;Accession: T46576
R;Yatzkan, B.; Yarden, O.
submitted to the EMBL Data Library, February 19
A;Description: Ppt-1, a N. crassa novel-type ph
A;Reference number: Z23089
A;Accession: T46576
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-479 < XAT>
A;Cross -references: UNIPARC:UPI000000D260; EMBL
C;Genetics:
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                                                                                                                                                          AGVWFGPDVTDNFLQRHRLSYVIRSHECKPNGHBFWHDNKIITIFSASNYYAIGSNKGAY
                                                                                                                                                                                                                 DDNVTLDDIRKLDRHKQ-----KQPGQAG------LMMEMLWTDPQPFPGRGPSK-RG
                                                                                                                                                                                                                                                                       SDSTSLDLIKSIDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMGCVPNTLRG
INIGPDYKLKFSQF
                                                   IRLINIQLMPHPVQY
                                                                                                          VGMQFGPDVTKRFCDKNGLEAIIRSHEVRMDGYEBEHDGKCITVFSAPKYCDMTENKGAY
                                                                                                                                                                                                                                                                                                                              RGNHETDDMNRVYGFEGECKHKY---NERTYKLFSESFSALPLATLIGKKFLVLHGGLFS
                                                                                                                                                                                                                                                                                                                                                                                  RGNHEDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLFLGSVLNSRVLIVHGGF--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDLHGKLDDLLVVLHKNGLPSSSNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLN
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456
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Pred. No. 1.8e-26;
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Churcher, 1998

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A;Map position: 2

C;Superfamily: protein phosphatase 5; phosphoesterase core homology; phosphoprotein; C;Superfamily: protein; mucleus; phosphoric monoester hydrolase; zinc C;Keywords: iron; metalloprotein; mucleus; phosphoric monoester hydrolase; zinc F;5-38/Domain: tetratricopeptide repeat homology <TT1>
F;39-72/Domain: tetratricopeptide repeat homology <TT2>
F;39-72/Domain: tetratricopeptide repeat homology <TT3>
F;179-444/Domain: phosphoprotein phosphatase homology <PPP>
F;211-280/Domain: phosphoesterase core homology <PPP>
F;211-280/Domain: phosphoesterase core homology <PPC>
F;217,219,246/Binding site: iron (Asp, His, Asp) #status predicted
F;246,278,327,404/Binding site: xinc (Asp, His, His, His, His) #status predicted
F;249,279,428/Active site: Asp, His, Tyr #status predicted
F;250,377/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                         phosphoprotein phosphatase (EC 3.1.3.16) PPTI - yeast (Saccharomyces cerevisiae) N/Alternate names: protein G6347; protein YGR123c; serine/threonine phosphatase C;Species: Saccharomyces cerevisiae C;Species: Saccharomyces cerevisiae C;Pate: 03-Aug-2001 #sequence revision 03-Aug-2001 #text_change 09-Jul-2004 C;Pate: 03-Aug-2001 #sequence revision 03-Aug-2001 #text_change 09-Jul-2004 C;Accession: S52571, S55981; S64432; S64697 R;Chen, M.X.; McPartlin, A.E.; Brown, L.; Chen, Y.H.; Barker, H.M.; Cohen, P.T.W SMBO J. 13, 4278-4290, 1994 RyTitle: A novel human protein serine/threonine phosphatase, which possesses fou A;Reference number: S52570; MUID:95009929; pMID:7925273 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession: S52571 A;Accession
A;Cross-references: UNIPROT:P53043; UNIPARC:UPI0000053298
R;van Dyck, L.; Goffeau, A.
submitted to the EMBL Data Library, December 1994
A;Description: Genes for an asn synthase, a GLFG-motif nu
e new ORFs, remnants of Ty and three tRNA genes.
A;Reference number: S55976
A;Accession: S55981
A;Molecule type: DNA
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;Residues: 1-473 <LYN>
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                                                                                                                         nase, a GLFG-motif nucleoporin
tRNA genes.
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RESULT T51611

phosphoprotein phosphatase (BC 3.1.3.16) PP7 [imported] - C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_c C;Accession: T51611

#text\_change 09-Jul-2004

Arabidopsis thaliana

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C;Superfamily: protein phosphatase 5; phosphoesterase core homology; phosphoprotein C;Keywords: iron; metalloprotein; nucleus; phosphoric monoester hydrolase; zinc F;12-4s/Domain: tetratricopeptide repeat homology <TT2> F;46-79/Domain: tetratricopeptide repeat homology <TT2> F;90-113/Domain: tetratricopeptide repeat homology <TT3> F;209-475/Domain: phosphoprotein phosphatase homology <PRC> F;243-312/Domain: phosphoprotein phosphatase homology <PRC> F;243-313/Domain: phosphoprotein phosphatase homology <PRC> F;243-312/Domain: phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein phosphoprotein 
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A; Gene: SGD: PPT1
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A;Residues: 1-380,'HHLE',389,'AP',392-393,'NFYGRTHKKPTGWVL',409,'SVV' <CHW>
A;Cross-references: UNIPARC:UPI0000168BE1; EMBL:X89417; NID:g897805; PID:g897806
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A; Accession: 864697
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A;Description: A novel human protein serine/threonine phosphatase, which possesses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPARC:UPI0000053298; EMBL:Z72908; NID:g1323200; PID:e243462; A;Experimental source: strain S288C
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A; Accession: S64432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Residues: 1-513 < VAW>
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Matches 130
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KIFRSHELRMGGVQFEQKGKLMTVFSAPNYCDSQGNLGGVIHV
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B.; Talla, E.; Nawrocki,
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R;Cannieux, M.; Chenieux, J.C.; Rideau, M.; Hamdi, S.
Plant Physiol. 118, 1533, 1998
A;Title: cDNA isolation of two serine/threonine phosphatases (PP1 and PP2A) from Cathars A;Reference number: Z16912; MUID:99139832; FMID:9988639
A;Reference number: Z16912; MUID:99139832; FMID:9988639
A;Recession: T09995
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-326 <CAN>
A;Residues: 1-326 <CAN>
A;Cross-references: UNIPROT:081955; UNIPARC:UPI00000A8113; EMBL:AJ007332
A;Experimental source: cell line C20D
C;Genetics:
A;Gene: pp1a
C;Function:
A;Description: catalyzes hydrolysis of peptidyl-phosphoserine or -phosphothreonine to re
C;Superfamily: serine/threonine protein phosphatase; bhosphoesterase core homology; phos
C;Keywords: phosphoric monoester hydrolase; serine/threonine-specific phosphatase
P;26-285/Domain: phosphorotein phosphatase homology <PPD>
F;54-122/Domain: phosphoesterase core homology <PPD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Andreeva, A.V.; Evans, D.B.; Hawes, C.R.; Bennett, N.; Kutuzov, M.A. Biochem. Mol. Biol. Int. 44, 703-715, 1998
A;Title: PP7, a plant phosphatase representing a novel evolutionary bra A;Reference number: Z25411
A;Accession: T51611
A;Accession: T51611
A;Status: preliminary; translated from GB/EWBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-413-(AND)
A;Cross-references: UNIPROT:049346; UNIPARC:UPI00000ACCB3; EMBL:AJ00005
A;Experimental source: cultivar Columbia; whole plants; 3 weeks old; g1
C;Function:
A;Description: catalyzes the hydrolytic dephosphorylation of protein-pic,Keywords: phosphoric monoester hydrolase; serine/threonine-specific;
                                                                                                                                                                                                                                                                                                                                                                                                                phosphoprotein phosphatase (EC 3.1.3.16) la catalytic chain - Ma Nalternate names: PPIA protein C;Species: Catharanthus roseus (Madagascar periwinkle) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change C;Accession: T09995
R;Cannieux, M.; Chenieux, J.C.; Rideau, M.; Hamdi, S. Plant Physiol. 118, 1533, 1998
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Best Local S
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117; Conserv
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                   12.8%;
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                   Score 441; DB 2
Pred. No. 2e-20;
    Mismatches
                                      DB 2;
    125;
                                      Length 326;
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phosphoprotein phosphatase (BC 3.1.3.16) PP1 - kidney bean
C;Species: Phaseolus vulgaris (kidney bean)
C;Date: 08-May-1995 #sequence revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: $60053, $52371
R;Zimmerlin, A; Jupe, S.C.; Bolwell, G.P.
Plant Mol. Biol. 28, 363-368, 1995
A;Title: Molecular cloning of the cDNA encoding a stress-inducible protein phosphatase A;Reference number: $60053; MUID:95359396; PMID:7632908
A;Accession: $60053
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr A;Molecule type: mRVA
A;Residues: 1-314 <272>
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F;52-120/Domain: phosphopsterase core homology <PPC>
F;52-120/Domain: phosphoesterase core homology <PEC>
F;58,60,86/Binding site: iron (Asp, His, Asp) #status predicted
F;86,118,167,242/Binding site: iron (Asp, Asn, His, His) #status predicted
F;89,119,266/Active site: Asp, His, Tyr #status predicted
F;90,215/Binding site: substrate phosphate (Arg) #status predicted
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Best Local
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                                                                          PGPDVTDNPLQRHRLSYVIRSHBCKPNGHBPMHDNKIITIPSASNYYAIGSNKGAYIRLN 398
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31.5%; Prer
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Pred. No. 3.7e-20;
3; Mismatches 116
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Cell 57, 997-1007, 1989
A;Title: The fission yeast dis2(+) gene required for chromosome disjoining encodes one c A;Reference number: A32550; MUID:89288305; PMID:2544298
A;Reference number: A32550; MUID:89288305; PMID:2544298
A;Accession: A32550
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-327 <OHK>
A;Cross-references: UNIPROT:P13681; UNIPARC:UPI0000131FAB; GB:M27068; NID:g341615; PIDN:
R;Lyne, M.; Rajandream, M.A.; Baxrell, B.G.; Wedler, H.; Kutzner, M.; Wambutt, R.
R;Lyne, M.; Rajandream, M.A.; Baxrell, B.G.; Wedler, H.; Kutzner, M.; Wambutt, R.
R;Lyne, M.; Rajandream, M.A.; Baxrell, B.G.; Wedler, H.; Kutzner, M.; Wambutt, R.
R;Lyne, M.; Rajandream, M.A.; Baxrell, B.G.; Wedler, H.; Kutzner, M.; Wambutt, R.
R;Lyne, M.; Rajandream, M.A.; Baxrell, B.G.; Wedler, H.; Kutzner, M.; Wambutt, R.
R;Lyne, M.; Rajandream, M.A.; Baxrell, B.G.; Wedler, H.; Kutzner, M.; Wambutt, R.
R;Lyne, M.; Rajandream, M.A.; Baxrell, B.G.; Wedler, H.; Kutzner, M.; Wambutt, R.
R;Lyne, M.; Rajandream, M.A.; Baxrell, B.G.; Wedler, H.; Kutzner, M.; Wambutt, R.
A;Residues: 1-327 <INN-
A;Residues: L.327 <INN-
A;Res
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Best Local Similarity
Matches 107; Conserv
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288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
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                                                                                                                                                                                                                                                                                                         DLIKSIDRGKYVSILRPPLTDGBPLDKTBWQQIPDIMWSDPQATMGCVPNTLRGAGVWFG
                                                                                                                                                                                                                                                                                                                                                                          CASINRIYGFYDECKRRY--NIKLWKTFTD-CFNCLPIAAIIDEKIFTMHGGLSPDLNSM
                                                                                                                                                                                                                                                                                                                                                                                                                                     DSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGFS-DSTSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LDSIIDRLLEVRGSR-PGRQVQLSEDEIRFLCNKAREIFISQPILLELEAPLKICGDIHG
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   LLCSP-QILKPASK-
                                                          LMPHFVQYISAASQTKRLSFKQRMGIVESS
                                                                                                                                                                                PDVTDNFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRLNNQ 400
                                                                                                                                                                                                                                                     DQIQRIMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QYYDLLRLFEYGGFPPEAN-YLFLGDYVDRGKQSLEVICLLLAYKIKYPENFFILRGNHE
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                                                                                                                     PDVVSRFLHKHDMDLVCRAHQVVEDGYEFFSKRQLVTLFSAPNYCGEFDNAGAMMSVDES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 435.5; DB 2;
; Pred. No. 4.5e-20;
62; Mismatches 130;
   KORYGYOGSS
                                                                                                                                                                                                                                                     PTDVPDTGLLCDLLWSDPDKDLTGWGDNDRGVSFTFG
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probable phosphoprotein phosphatase (BC 3.1.3.16) F21B7.27 - C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_chan C;Accession: T00913 R;Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y eologis, A.; Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBI Data Library, January 1998
A;Description: Genomic sequence for Arabidopsis t
A;Reference number: Z14208
A;Accession: T00913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Introns: 118/1; 138/2; 164/3; 189/2; 221/1; 230/3; 262/3; C;Superfamily: serine/threonine procein phosphatase, BSUI to C;Keywords: phosphoric monoester hydrolase C;Keywords: phosphoric monoester hydrolase F;412-684/Domain: phosphoprotein phosphatase homology <PPP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: translated from A;Molecule type: DNA A;Residues: 1-729 <SHI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPARC:UPI0000175984; EMBL:AC002560; NID:g2618677; PID:g2809258
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Best Local Similarity
Matches 98; Conserv
17
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                                                                       FADGRLITVFSATNYCGTAQNAGAILVIGRDMVIYPKLIHPH
                                                                                                                          MHDNKITIFSASNYYAIGSNKGAYIRLNNQLM-----PH
                                                                                                                                                                                                                                  FDIMWSDP---QATMCCVPNTLRGAG-VWFGPDVTDNFLQRHRLSYVIRSHBCKPNGHEF
                                                                                                                                                                                                                                                                                                                                       YRWLPLGSVLNSRVLIVHGGFSDSTSLDLIKSIDRGKYVSILRPPLTDGEPLDKTEWQQI
                                                                                                                                                                                                                                                                                                                                                                                              IMLLFALKIEYPKNIHLIRGNHESLAMNRIYGFLTECBERMGESY----GFEAWLKINQV
                                                                                                                                                                                                                                                                                                                                                                                                                                             LLLLLSLYLAFPNAVFLNRGNHEDSVMNARYGFIREVESKYPRNHKRILAF----IDEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVSTAVSQQVTVCGDLHGKLDDLLVVLHKNGLPSSSN-----PYVFNGDFVDRGKRGLEV
                                                                                                                                                                                    KDILWSDPTMNDTVLGIVDNA-RGEGVVSFGPDIVKAFLERNGLEMILRAHECVIDGFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTLLQLKVPIKVFGDIHGQYGDLMRLFHEYGHPSVEGDITHIDYLFLGDYVDRGQHSLEI
                                                                                                                                                                                                                                                                                      FDYLPLAALLEKKVLCVHGGIGRAVTIEEIENIE-----RPAFPD-----TGSMVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 434; DB 2;
Pred. No. 1.7e-19;
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RESULT T09544

C;Genetics:
A;Gene: PP1 beta
C;Function. A;Description: catalyzes hydrolysis of peptidyl-phosphoserine or -phosphothreonine to C;Superfamily: serine/threonine protein phosphatase; phosphoesterase core homology; ph C;Keywords: phosphoric monoester hydrolase; serine/threonine-specific phosphatase F;26-285/Domain: phosphoprotein phosphatase homology <PPP>
F;54-122/Domain: phosphoesterase core homology <PEC> A; Molecule type: mRNA A; Residues: 1-326 < VIS> Arch. Biochem. Biophys. 360, 206-214, 1998
A; Title: Protein phosphotase 1 catalytic subunit isoforms
A; Reference number: Z16730; MUID:99068922; PMID:9851832
A; Accession: T09544 phosphoprotein phosphatase (BC 3.1.3.16), catalytic beta chain - alfalfa C;Species: Medicago sativa (alfalfa) C;Species: Medicago sativa (alfalfa) C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-20 C;Accession: T09544 A; Cross-references: UNIPROT: 065844; ; Accession: T09544 ; Vissi, E.; Csordas Toth, Query Match Best Local Similarity Matches 102; Conserv 12.6%; E.; Kovacs, Score 433.5; Pred. No. 6e UNIPARC: UPI00000A4B32; I.; Magyar, DB 2; Z.; Horvath, Length EMBL: AJ002485; alfalfa: Biochemical G.; Bagossi, 09-Jul-2004 NID: 93176071, P.,

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Mismatches

37;

Gaps

7;

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6e-20;

RESULT 16

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Cell 57, 987-996, 1989
A, Title: The bimG gene of Aspergillus nidulans, required for completion of anaphase, enc A, Title: The bimG gene of Aspergillus nidulans, required for completion of anaphase, enc A, Steference number: A32549; MUID:89288304; PMID:2544297
A, Accession: A32549
A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-323 < DOO>
A, Residues: 1-323 < DOO>
A, Cross-references: UNIPROT:P20654; UNIPARC:UPI0000131FBC; GB:M27067; NID:g532580; PIDN:C; Superfamily: serine/threonine protein phosphoric monoseter hydrolase; serine/threonine-specic; Steywords: iron; metalloprotein; phosphoric monoseter hydrolase; serine/threonine-specic; 29-288/Domain: phosphosporotein phosphatase homology < PPP>
F; 57-125/Domain: phosphosporotein phosphatase core homology < PPP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphoprotein phosphatase (EC 3.1.3.16) bimG - Emeri N;Alternate names: mitosis protein bimG C;Species: Emericella nidulans, Aspergillus nidulans C;Date: 05-Oct-1989 #sequence_revision 05-Oct-1989 #t C;Accession: A32549 E;Doonan, J.H.; Morris, N.R.
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99; Conser
                                                                                                                                                                                                                                                                                 IDLLIDVFRKKRGNRLHPKYVALI---LREAAKSLKQLPNISPVSTAVSQQVTVCGDLHG
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PDVTDNFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRLNNQ
                                                                                                             DLIKSIDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMGCVPNTLRGAGVWFG
                                                                                                                                                             CASINRIYGFYDECKRRY--NIKLWKTFTD-CFNCLPIAAIIDEKIFTMHGGLSPDLNSM
                                                                                                                                                                                                        DSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGFS-DSTSL
                                                                                                                                                                                                                                                     QYYDLLRLFEYGGFPPEAN-YLFLGDYVDRGKQSLETICLLLAYKIKYPENFFVLRGNHE
                                                                                                                                                                                                                                                                                                                                             LDSTIDRLLEVRGSR-PGKQVQLLESEIRYLCTKAREIFISQPILLELEAPIKICGDIHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PNAVFLNRGNHEDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLI
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                                                                     EQIRRVMR--
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Pred. No. 1.1e-19;
6; Mismatches 127;
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submitted to the EMBL Data Lib
A;Reference number: Z21985
A;Accession: T41293
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A;Accession: Bazzara, A;Status: preliminary A;Status: preliminary A;Nolecule type: DNA A;Nolecule type: DNA A;Residues: 1-322 <OHK>
A;Cross-references: UNIPROT:P23880; UNIPARC:UPI0000131FB0; A;Cross-references: UNIPROT:P23880; UNIPARC:UPI0000131FB0; A;Cross-references: UNIPROT:P23880; UNIPARC:UPI0000131FB0; A;Cross-references: UNIPROT:P23880; UNIPARC:UPI0000131FB0; A;Cross-references: UNIPROT:P3880; UNIPARC:UPI00000131FB0; A;Cross-references: UNIPROT:P3880; UNIPARC:UPI0000131FB0; A;Cross-references: UNIPROT:P3880; UNIPARC:UPI00000131FB0; A;Cross-references: UNIPROT:UPI00000131FB0; A;Cross-references: UNIPROT:UPI00000131FB0; A;Cross-reference
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-322 < MOO>
A; Cross-references: UNIPARC: UPI0000131FB0; EMBL: AL031824; PIDN: CAA21222.1; GSPDB: GN00066
A; Experimental source: strain 972h-; cosmid c31H12
C; Genetics:
A; Genetic
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C;Accession: B32550; T41275
R;Ohkura, H.; Kinoshita, N.; Miyatani,
R;Ohkura, H.; Kinoshita, N.; Miyatani,
R;Ohkura, H.; Kinoshita, N.; Miyatani,
R;Ohkura, H.; Kinoshita, N.; Miyatani,
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N;Alternate names: suppressor protein sds21
C;Species: Schizosaccharomyces pombe
C;Date: 12-Oct-1999 #sequence revision 12-Oct-1989
C;Accession: B32550; T41293
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A;Title: The fission yeast dis2(+) gene required for chromosome
A;Reference number: A32550; MUID:89288305; PMID:2544298
A;Accession: B32550
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LMPHFVQYISAASQTKRLSFKQRMGIVESSALKE 434
                                                                                                                                              ADVVSRFLQKHDLDLICRAHQVVBDGYBFFGKRQLVTIFSAPNYCGBFDNVGAMMSVNBD
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Pred. No. 1.1e-19;
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Plant Mol. Biol. 21, 307-316, 1993

Plant Mol. Biol. 21, 307-316, 1993

A;Title: Expression of multiple type 1 phosphoprotein phosphatases in Arabidopsis thalia A;Reference number: S31085; MUID:93144705; PMID:7878768

A;Reference number: S31085 MUID:93144705; PMID:7878768

A;Accession: S31085

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-290, 78', 292-318 <SM11>
A;Cross-references: UNIFARC:UPI0000175978; EMBL:M93408

A;Cross-references: UNIFARC:UPI0000175978; EMBL:M93408; MID:9166571; PIDN:AAA32723.1; PIR;Smith, R.D.; Walker, J.C.

submitted to the EMBL Data Library, May 1992

A;Reference number: S49037

A;Mccession: S49037

A;Mccession: S49037

A;Mccession: S49037

A;Gross-references: UNIFARC:UPI0000175977; EMBL:M93408; NID:9166571; PIDN:AAA32723.1; PIR; Pin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

R;Jin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

R;Jin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Traser, C.M.; Venter, J. C.M.; Venter, J. C.M.; Venter, J. C.R.; Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 402, 761-768, 1999

A, Title: Sequence and analysis of chromosome 2 of A; Reference number: A84420; MUID:20083487; PMID:10 A; Accession: H84695

A; Status: preliminary A; Molecule type: DNA A; Residues: 1-318 <570>
A; Cross-references: UNIPARC:UPI0000175977; GB:AE00 C; Genetics: C; Superfamily: serine/threonine protein phosphatas C; Keywords: iron; metalloprotein; phosphoric monoe C; Keywords: iron; metalloprotein; phosphatas homology <-PE + 13-30/Lomain: phosphoprotein phosphatas homology <-PE + 177, 79, 105/Binding site: iron (Asp, His, Asp) #st F; 105, 138, 284/Active site: Asp, His, Tyr #status p F; 109, 233/Binding site: substrate phosphate (Arg)
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A;Cross-references: UNIPARC:UPI0000175977;
A;Experimental source: clone PP1
R;Smith, R.D.; Walker, J.C.
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Best Local S
Matches 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Superfamily: serine/threonine protein phosphatase; phosphoesterase core homology; phosphords: iron; metalloprotein; phosphoric monoester hydrolase; serine/threonine-spec:,43-301/Domain: phosphoprotein phosphatase homology <PPP>
,71-139/Domain: phosphopsterase core homology <PEC>
,77-79,105/Binding site: iron (Asp, His, Asp) #status predicted
,105,137,186,260/Binding site: zinc (Asp, Asn, His, His) #status predicted
,105,137,186,260/Binding site: Asp, His, Tyr #status predicted
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Residues: 1-318 <NIT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233/Binding site: substrate phosphate (Arg)
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VLHKNGLPSSSNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNAR:
                                                                                                                                                                                                                                                                                       MAEKPAQEQEQKRAMEPAVLD-----DIIRRLVE
                                                                                                                                                                                                                                                                                                                                                                    MPQAAGRKNQYQGSAHVSVLDDKDDLVEEFGDIVNAKIELPIRKNHIDLLIDVFRKKR---
                                                                                                                                                                                                      -GNRLHPKYVALILREAAKSLKQLPNIS-----PVSTAVSQQVTVCGDLHGKLDDLLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                         12.4%; Score 428; DB 2; 29.6%; Pred. No. 1.3e-19; tive 67; Mismatches 121
                                                                                                                             -LSEG--EIRQLCAVSKEIFLQQPNLLELEAPIKICGDIHGQYSDLLR
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PMID:10617197
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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L.; Tallon, L
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phosphoprotein phosphatase (EC 3.1.3.16) F23B12.1 [similarity] - C;Species: Caenorhabditts elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change C;Accession: T21288
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A;Gene: nppl
C;Superfamily: serine/threonine protein phosphatase; phosphoesterase core homology; phos C;Keywords: iron; phosphoric monoester hydrolase; serine/threonine-specific phosphatase; F;41-300/Domain: phosphoprotein phosphatase homology <PPP>
F;69-137/Domain: phosphoesterase core homology <PEC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Suh, M.; Cho, H.; Kim, Y.; Liu, J.; Lee, H.
Plant Mol. Biol. 36, 315-322, 1998
A;Title: Multiple genes encoding serine/threonine protein
A;Reference number: Z14967; MUID:98145437; PMID:9484443
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A; Residues: 1-317 < SUH>
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R; Suh, M.; Cho, H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phosphoprotein phosphatase (EC 3.1.3.16) 1 - common tobacco C;Species: Nicotiana tabacum (common tobacco) C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change
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LVCRAHQVVBDGYEFFAERQLVTIFSAPNYCGEFDNAGAMMSVDESLMCSF
                                         YVIRSHECKPNGHEFWHDNKIITIFSASNYYAIGSNKGAYIRLNNQLMPHF 405
                                                                                                                                                                            KRRF---NVKLWKCFTECFNCLPVAALIDEKILCMHGGLSPVLTNLDQIRNLPR-----
                                                                                                                                                                                                                                                                                                       PSSSNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNARYGFIREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MPQAAGRKNQYQGSAHVSVLDDKDDLVEEFGDIVNAKIELPIRKNHIDLLIDVFRKKRGN 118
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                                                                                                                             LRPPLTDGEPLDKTEWQQI FDIMWSDPQATMGCVPNTLRGAGVWFGPDVTDNFLQRHRLS
                                                                                                                                                                                                                      ESKYPRNHKRILAFIDBVYRWLPLGSVLNSRVLIVHGGFSD-STSLDLIKSIDRGKYVSI
                                                                                                                                                                                                                                                                  PPEAN-YLFLGDYVDRGKQSLETICLLLAYKIKYPENFFLLRGNHECASINRIYGFYDEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                              MAQNNEQQQQGQGLIEAGVLD------DIINRLLE-----FRNARTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                        PTDVPDSGLLCDLLWSDPSREVKGWGMNDRGVSYTFGPDKVAEFLMQHDMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.4%; Score 426.5; 30.2%; Pred. No. 1.6
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#text\_change 05-Oct-2004

Caenorhabditis

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R;Wild, A.
submitted to the EMBL Data Library, July 1996
A;Reference number: Z19402
A;Reference number: Z19402
A;Recession: T21288
A;Accession: T21288
A;Accession: T21288
A;Accession: T21281
A;Cross-references: UNIPROT:Q27495; UNIPARC:UPI000007C7EF; EMBL:Z77659; PIDN:CAB01164.1;
A;Molecule type: DNA
A;Residues: 1-401 <WILL>
A;Cross-references: UNIPROT:Q27495; UNIPARC:UPI000007C7EF; EMBL:Z77659; PIDN:CAB01164.1;
A;Genetics:
C;Genetics:
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: serine/threonine protein phosphatase; phosphoesterase core homology; phos
C;Superfamily: serine/threonine protein phosphatase homology <PPP>
F;135-193/Domain: phosphoprotein phosphoric monoester hydrolase; serine/threonine-speci
F;97-356/Domain: phosphoprotein phosphoric monoester hydrolase; serine/threonine-speci
F;159,191,240,315/Binding site: iron (Asp, His, Asp) #status predicted
F;159,191,240,315/Binding site: iron (Asp, His, Asp) #status predicted
F;162,192,393/Accive site: Asp, His, Tyr #status predicted
F;162,192,393/Accive site: Asp, His, Tyr #status predicted
F:162,192,393/Accive site: Asp, His, Tyr #status predicted
phosphoprotein phosphatase (BC 3.1.3.16) 1 catalytic chain (clone TOPP2) - Arabidopsis t (.Species: Arabidopsis thaliana (mouse-ear cress)
C;Opecies: Arabidopsis thaliana (mouse-ear cress)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: 831086
R;Smith, R.D.; Walker, J.C.
Plant Mol. Biol. 21, 307-316, 1993
A;Title: Expression of multiple type 1 phosphoprotein phosphatases in Arabidopsis thalia A;Accession: S31085; MUID:93144705; PMID:7678768
A;Accession: S31085
A;Molecule type: mRNA
A;Residues: 1-312 <SMI>
A;Residues: 1-312 <SMI>
A;Cross-references: UNIPROT:P48482; UNIPARC:UPI00000BD80; EMBL:M93409; NID:9166796; PID:SUPErfamily: serine/threonine protein phosphoric monoester hydrolase; serine/threonine-specif;36-295/Domain: phosphoprotein phosphoric monoester hydrolase; serine/threonine-specif;36-295/Domain: phosphoprotein phosphatase homology <PPP>
F;64-132/Domain: phosphoprotein phosphatase core homology <PPP>
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113; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVVSKKIICMHGGISEDLIDLTQLEKIDR------PFDIPDIGVISDLTWA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KVKLDIEAPVKICGDIHGQFEDLMALFELNGWP-EEHKYLFLGDYVDRGPFSIEVITLLF
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F;700,72,98/Binding site: iron (Asp. His, Asp) #status predicted F;98,130,179,254/Binding site: iron (Rsp. Asn. His, His) #status pr F;101,131,778/Active site: Asp. His, Tyr #status predicted F;102,227/Binding site: substrate phosphate (Arg) #status predicted
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 QYQGSAHVSVLDDKDDLVEEFGDIVNAKIELPIRKNHIDLLIDVFRKKRG-----NRLH
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QVVEDGYEFFADRQLVTIFSAPNYCGEFDNAGAMMSVDESLMCSF-QILKPADRKPR
                                                                                                                            DGEPLDKTEWQQIFDIMWSDPQATMGCVPNTLRGAGVWFGPDVTDNFLQRHRLSYVIRSH
                                                                                                                                                                                                                 NHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGFS-DSTSLDLIKSIDRGKYVSILRPPLT
                                      BCKPNGHBFMHDNKIITIFSASNYYAIGSNKGAYIRLNNQLMPHFVQYISAASQTKR
                                                                                     ---PTDVPDSGLLCDLLWSDPSKDVKGWGMNDRGVSYTFGPDKVABFLIKNDMDLICRAH
                                                                                                                                                                      -SVRLWKVFTDSFNCLPVAAVIDDKILCMHGGLSPDLTNVEQIKNIKR
                                                                                                                                                                                                                                                            YLFLGDYVDRGKQSLETICLLLAYKIKYPENFFLLRGNHECASINRIYGFYDECKRRF--
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30.5%; Pred. No. 2.1e-19;
tive 63; Mismatches 128
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A; Reference number: Z16730; MUID:99068922; PMID: 0acince A; Status: T09550
A; Cross-references: UNIPROT:065847; UNIPARC:UPI00000AABFC; EMBL:AJ002488; NID:g3176077, A; Experimental source: subspecies sativa; strain RA3
C; Genetics:
A; Gene: Pp1 epsilon
C; Function:
A; Description: catalyzes hydrolysis of peptidyl-phosphoserine or -phosphothreonine to C; Superfamily: serine/threonine protein phosphatase; phosphoesterase core homology; ph C; Keywords: phosphoric monoester hydrolase; serine/threonine-specific phosphatase F; 42-301/Domain: phosphoprotein phosphatase homology <PPP>
F; 70-138/Domain: phosphoesterase core homology <PPC>
                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-323 <VIS>
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HEDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRMLFLGSVLNSRVLIVHGGFS-DST

278

219 77 Matches Query Match

106;

Conservative

20

VLDDIIRRLTBVRLSRPGKQVQLSBA--BIKQLCSASRDIFLQQPNLLBLBAPIKICGDI LLIDVFRKKRGNRLHPKYVALILREAAKSLKQLPNIS-----PVSTAVSQQVTVCGDL

HGKIDDLLVVLHKNGLPSSSNPYVFNGDFVDRGKRGLBVLLLLLSLYLAFPNAVFLNRGN

HGQYSDLLRLFEYGGLPPQSN-YLFLGDYVDRGKQSLETICLLLAYKIKYPENFFLLRGN

Local Similarity

12.2%;

Score 421; DB 2; Pred. No. 3.6e-19; Mismatches

Length 323

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Indels

30;

Gaps

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C;Accession: T09548
C;Accession: T09548
R;Vissi, E.; Csordas Toth, E.; Kovacs, I.; Magyar, Z.; Horvath, G.; Bagossi, P.; Gergely Arch. Biochem. Biophys. 360, 206-214, 1998
A;Title: Protein phosphotase 1 catalytic subunit isoforms from alfalfa: Biochemical char A;Accession: T09548
A;Ttle: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T09548
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-326 <VIS>
A;Cross-references: UNIPROT:065846; UNIPARC:UDI0000AAB92; EMBL:AJ002487; NID:g3176075;
A;Experimental source: subspecies sativa, strain RA3
C;Gene: PP1 delta
C;Gene: PP1 delta
C;Superfamily: serine/threonine protein phosphatase; phosphosetrase core homology; phosphoric monoester hydrolase; serine/threonine-specific phosphatase
C;Keywords: phosphoric monoester hydrolase; serine/threonine-specific phosphatase
F;26-285/Domain: phosphorotein phosphatase homology <PPP>
F;54-122/Domain: phosphoreterase core homology <PPP>
                                          RESULT 26
T03304
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probable phosphoprotein C; Species: Oryza sativa
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                                                                                                                                                                                                       YTFGADRVKEFLOKHDLDLICRAHOVVEDGYEFFANROLVTIFSAPNYCGEFDNAGAMMT
                                                                                                                                                                                                                                                                                     LHDLNQTKNLRR-------PCEVPESGLLCDLLWSDPSSDVRGWGESERGVS
                                                                                                                                                                                                                                                                                                                         STSLDLIKSIDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMGCVPNTLRGAG 336
                                                                                                                                                                                                                                                                                                                                                                   GNHECASINRIYGFYDECKRRY---NVKLWKMFTDCFNCLPVAALIDEKIICMHGGLSPE
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                                                                                                                                                                                                                                             VWFGPDVTDNFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIR 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INRLLEV-RGRPGKQVQ-----LSEA--BIKQLCLVSKDIFMNQPNLLKLEAPIKICG
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                                                                                                                       VNESLVCSF-QILKPLDKKPKFSFGSTTTVKSSSPTK
                                                                                                                                                             LNNQLMPHFVQYISAASQTKRLSFKQRMGIVESSALK 433
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  phosphatase (rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 421; DB 2;
Pred. No. 3.6e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---PVPIPDTGLLRDQFWSDHGKDVKGWGMNDRGVSYT
                     (EC
                     3.1.3.16)
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                     1 catalytic
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C;Superfamily: serine/threonine protein phosphatase; phosphoesterase core homology; phosphorods: iron; metalloprotein; phosphoric monoester hydrolase; serine/threonine-speci F;7-268/Domain: phosphorotein phosphatase homology <PPD>
F;35-103/Domain: phosphoseterase core homology <PEC>
F;41-3,69/Binding site: iron (Asp. His, Asp.) #status predicted
F;69,101,151,227/Binding site: zinc (Asp. Asn. His, His) #status predicted
F;72,102,251/Acctive site: Asp. His, Tyr #status predicted
F;73,200/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphoprotein phosphatase (BC 3.1.3.16) 1 F25B3.4 C; Species: Caenorhabditis elegans C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Experimental source; seed C;Superiamily: serine/threonine protein phosphatase; phosphoesterase C;Keywords: phosphoric monoester hydrolase C;Keywords: phosphoric monoester hydrolase F;36-295/Domain: phosphoprotein phosphatase homology <PPP>F;64-132/Domain: phosphoesterase core homology <PEC>
                                                                                                                                                                                A; Map position: 5
A; Introns: 20/2; 157/3;
C; Superfamily: serine/tl
                                                                                                                                                                                                                                                                                       A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q27496; UNIPARC:UPI000007D589; EMBL:Z70752; A;Experimental source: clone F25B3
                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-291 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: Z19406
A;Accession: T21322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Gardner, A. submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-317 <WAN>
A;Cross-references: UNIPROT:P48489; UNIPARC:UPI0000131FBF; EMBL:U31773; NID:g951335; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
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A; Accession: T03304
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R;Wang, B.; Chang, M.; Chen, X.; Wu, R.
submitted to the EMBL Data Library, July 1995
                                                                                                                                                                                                                                                             A;Gene: CESP:F25B3.4
                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: translated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: T21322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGFS-DSTS
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31.6%;
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Pred. No. 3.8e-19;
L; Mismatches 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          April
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [similarity]
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A;MAD position: 2

A;MAD position: 2

A;MAD position: 2

A;Introns: 73/1; 259/3

C;Superfamily: serine/threonine protein phosphatase; phosphoesterase core homology; phosphorous: iron; metalloprotein; phosphoric monoester hydrolase; serine/threonine-specif; Keywords: iron; metalloprotein phosphatase homology <PPP>
F;40-299/Domain: phosphoprotein phosphatase homology <PPP>
F;68-136/Domain: phosphoesterase core homology <PEC>
F;74-76,102/Binding site: iron (Asp, His, Asp) #status predicted
F;102,134,183,258/Binding site: zinc (Asp, Asn, His, His) #status predicted
F;105,135,282/Active site: Asp, His, Tyr #status predicted
F;105,31/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, L. euss, D.; Mierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C. Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P48484; UNIPARC:UPI0000131FB4; EMBL:M93411; NID:g166800; R;Rounsley, S.D.; Lin, X.; Ketchum, Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; I submitted to the EMBL Data Library, November 1997
A;Description: Arabidopsis thaliana chromosome II BAC T517 genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plant Mol. Biol. 21, 307-316, 1993

A;Title: Expression of multiple type 1 phosphoprotein phosphatases
A;Reference number: S31085; MUID:93144705; PMID:7678768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphoprotein phosphatase (EC 3.1.3.16) 1 catalytic chain (clone TOPP4) - N,Alternate names: hypothesin nt2339840; protein TSI7.14 C;Species: Arabidopsis thaliana (mouse-ear crees) C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 09-Jul-2004 C;Accession: S31088; T01014 B84822
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Sequence and analysis of chromosome A;Reference number: A84420; MUID:20083487; PA;Accession: B84822
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A; Residues: 1-321 <STO>
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A; Residues: 1-321 < SMI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Smith, R.D.; Walker,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 94
                                                                                                                                                                                                                                                                                               ;Gene: At2g39840; T5I7.14
                                                                                                                                                                                                                                                                                                                        Genetics:
                                                                                                                                                                                                                                                                                                                                            ;Cross-references: UNIPARC:UPI0000131FB4; GB:AE002093; NID:g2642169; PIDN:AAB87136.1;
                                                                                                                                                                                                                                                                                                                                                                                                                             Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Experimental source: cultivar Columbia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: DNA
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Pred. No. 3.6e-19;
8; Mismatches 107
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PMID:10617197
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A;Molecule type: DNA
A;Residues: 1-310 <JOH>
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A;Residues: 1-310 <JOH
A;Residues: Identification: 4
A;Resperimental source: strain Bristol N2; clone ZK354
C;Genetics: 4
A;Residues: CESP: ZK354.9
A;Map position: 4
A;Introns: 27/2
C;Resperimental: 27/2
C;R
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T25993
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A;Reference number: Z20120
A;Accession: T25993
A;Status: translated from GB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Johnson, D.; Wamsley, P.; Bradshaw, H. submitted to the EMBL Data Library, Pebrua A;Description: The sequence of C. elegans
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Matches 104; Conserv
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Best Local Similarity
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NRGNHEDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLFLGSVLNSRVLIVHGG---
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                                                                                                          CGDIHGQFSDLLRLFDKNGFPHRAN-YLFLGDYVDRGKHCLETILLLFAYKVIFPNHFFM
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                                                                                                                                                                                                                                                                                                                                                                                                          Score 418.5; DB 1
Pred. No. 4.9e-19;
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Pred. No. 4.4e-19;
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A;Map position: i
A;Introns: 59/3
C;Function:
A;Description: pl
C;Superfamily: se
C;Keywords: iron
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S32595
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A;Molecule type: DNA
A;Residues: 1-272,'V',274-312 <OHK>
A;Residues: 1-272,'V',274-312 <OHK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ribietrich, F.S.
Ribietrich, F.S.
Ribietrich, F.S.
Submitted to the EMBL Data Library, December
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J. Biol. Chem. 266, 23796-23801, 1991
A;Title: The yeast GLC7 gene required for glycogen accumulation encodes a type 1 protein A;Reference number: S32595; MUID:92084672; PMID:1660885
A;Accession: S32595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosphoprotein phosphatase (BC 3.1.3.16) 1 catalytic chain - yeast (Saccharomyces N;Alternate names: Chromosome disjoining protein DIS2S1; protein YER133W C;Species: Saccharomyces cerevisiae C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 09-Jul-2004 C;Accession: 832595, 830854; 850636; 832550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPARC:UPI0000052DD3; EMBL:U18916; NID:g1384128; PIDN:AAC03231 R;Ohkura, H.; Kinoshita, N.; Miyatani, S.; Toda, T.; Yanagida, M. Cell 57, 997-1007, 1989 Cell 57, 997-1007, 1989 A;Title: The fission yeast dis2(+) gene required for chromosome disjoining encodes A;Reference number: A32550; MUID:89288305; PMID:2544298 A;Accession: E32550
                                                                                                                                                                                                                                                                                                                                                                A;Gene: SGD:GLC7; DIS2S1
A;Cross-references: SGD:
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A; Residues: 1-312 < FEN>
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                                                              Nipescription: phosphoric monoester hydrolase; serine/threonine-specific phosphatase; Superfamily: serine/threonine protein phosphatase; phosphoesterase core homology; phosphatase iron; metalloprotein; phosphoric monoester hydrolase; serine/threonine-specific-29-288/Domain: phosphoprotein phosphatase homology <PPP>
757-125/Domain: phosphoprotein phosphatase homology <PPP>
763.65,91/Binding site: iron (Asp. His, Asp) #status predicted
791.123,172,247/Binding site: Zinc (Asp. Asn, His, His) #status predicted
794.124,271/Active site: Asp, His, Tyr #status predicted
795,220/Binding site: substrate phosphate (Arg) #status predicted
Query Match
Best Local Similarity
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12.2%;
Score 418.5; DB 2;
Pred. No. 4.9e-19;
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NHKRILAFIDEVYRWLFLGSVLNSRVLIVHGGFS-DSTSLDLIKSIDRGKYVSILRPPLT
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YLFLGDYVDRGKQSLETICLLLAYKIKYPENFFLLRGNHBCASINRIYGFYDBCKRRF--

150

-SVRLWKVFTDSFNCLPVAAVIDDKILCMHGAISPDLTNVEQIKNIKR---

93

198

DGEPLDKTEWQQIFDIMWSDPQATMGCVPNTLRGAGVWFGPDVTDNFLQRHRLSYVIRSH
---PTDVPDSGLLCDLLWSDPSKDVKGWGMNDRGVSYTFGPDKVABFLIKNDMDLICRAH

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A;Accession: $24264
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-312 <FER>
A;Cross-references: UNIFROT:P48482; UNIPARC:UPI000016DBB8; EMBL:Z12163; NID:g16432; PIDN
C;Superfamily: serine/threonine protein phosphatase; phosphoesterase core homology; phos
C;Keywords: iron; metalloprotein; phosphoric monoester hydrolase; serine/threonine-speci
F;36-295/Domain: phosphoprotein phosphatase homology <PPE>
F;64-132/Domain: phosphoesterase core homology <PEC>
F;70,72,98/Binding site: iron (Asp, His, Asp) #status predicted
F;98,130,179,254/Binding site: iron (Asp, Asn, His, His) #status predicted
F;101,131,278/Active site: Asp, His, Tyr #status predicted
F;101,131,278/Active site: substrate phosphate (Arg) #status predicted
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A;Description: Molecular characterization of protein phosphatases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phosphoprotein phosphatase (BC 3.1.3.16) IA catalytic chain - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S24264
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YVFNGDFVDRGKRGLEVLLLLSLYLAFFNAVFLNRGNHEDSVMNARYGFIREVESKYFR
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                                                                                                                                PKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLLVVLHKNGLPSSSNP
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                                                                                                                                                                                                                                                                                               12.2%; Score 418.5; DB 2; 30.3%; Pred. No. 4.9e-19; tive 63; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63,
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C;Accession: T09547

R;Vissi, E.; Csordas Toth, B.; Kovacs, I.; Magyar, Z.; Horvath, G.; Bagossi, P.; Gergely Arch. Biochem. Biophys. 360, 206-214, 1998

A;Title: Protein phosphotase 1 catalytic subunit isoforms from alfalfa: Biochemical char A;Reference number: Z16730; MUID:99068922; PMID:9851832

A;Accession: T09547

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-325 <VIS>
A;Cross-references: UNIPROT:065845; UNIPARC:UPI00009DAB2; EMBL:AJ002486; NID:g3176073;
A;Experimental source: subspecies sativa, strain RA3

C;Genetics:
A;Gene: PP1 gamma

C;Gunction:
A;Description: catalyzes hydrolysis of peptidyl-phosphoserine or -phosphothreonine to re
C;Superfamily: serine/threonine protein phosphatase; phosphotesterase core homology; phos
C;Keywords: phosphoric monoester hydrolase; serine/threonine-specific phosphatase
F;25-284/Domain: phosphoprotein phosphatase homology <PPP>
F;33-121/Domain: phosphoesterase core homology <PPE>
submitted to the EMBL Data L
A;Reference number: Z19047
A;Accession: T18936
A;Status: preliminary; trans
A;Molecule type: DNA
A;Residues: 1-401 <WIL>
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C;Species: Medic
C;Date: 16-Jul-1
C;Accession: TOS
                                                                                                                                 phosphoprotein phosphatase (EC 3.1.3.16) 1-beta catalytic chain - Caenorhabditis C,Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T18936; T25398 R;McMurray, A.
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                                                                                                                                                                                                                                                                                                                                                                                  SNYYAIGSNKGAYIRLNNQLMPHFVQYISAASQTKRLSF 420
                                                                                                                                                                                                                                                                                                                                                                                                                                    SKDVQGWGMNDRGVSYTFGADKITEFLEKHDLDLICRAHQVVEDGYEFFANRQLVTIYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QATMGCVPNTLRGAGVWFGPDVTDNFLQRHRLSYVIRSHECKPNGHBFMHDNKIITIFSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSLYLAFPNAVFLNRGNHEDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - PVSTAVSQQVTVCGDLHGKLDDLLVVLHKNGLPSSSNPYVFNGDFVDRGKRGLEVLLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIVNAKIELPIRKNHIDLLIDVFRKKRGNRLHPKYVALILREAAKSLKQLPNIS-----
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                                                                                                              June
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A;Residues: 1-401 <WIZ>
A;Cross-references: UNIPARC:UPI00000787E1; EMBL:Z73977; PIDN:CAA98291.1; GSPDB:GN000
A;Cross-references: UNIPARC:UPI00000787E1; EMBL:Z73977; PIDN:CAA98291.1; GSPDB:GN000
A;Genetics:
C;Genetics: CESP:CO5A2.1
A;Gene: CESP:CO5A2.1
A;Map position: 5
A;Introns: 47/2; 120/1; 159/3; 197/1; 351/3
A;Introns: 47/2; 120/1; 159/3; 197/1; 351/3
A;Introns: 47/2; 120/1; 159/3; 197/1; 351/3
C;Superfamily: serine/threonine protein phosphoric monoester hydrolase; serine/threonine-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-series-s
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A;Reference number: Z20028
A;Accession: T25398
A;Status: preliminary; translated from
A;Molecule type: DNA
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A;Experimental source: clone C05A2
R;Kelly, P.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 HPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLLVVLHKNGLPSSSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 QAAGRKNQYQGSAHVSVLDDKDDLVBBFGDIVNAKIBLPIRKNHIDLLIDVFRKKRGNRL
                                                                                                                                                                                GHQVVEDGYEFFGRRGLVTVFSAPNYCGEFDNAGAVMNVDENLLCSF-QILKPQSQLVMD
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AALAEKONNFVANLAGMANIKIEOKP-OPMIOKRFRR
                                                                                     KRLSFKQRMGIVESSALKELAVRMRDHRDELEDEFRK 452
                                                                                                                                                                                                                                                                                                                                                           ----PCDVQETGLLCDVLWSDPDATVVGWAPNB-RGVSYVFGVDVLAQFLQKMDLDIVVR
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phosphoprotein phosphatase (EC 3.1.3.16) 1-alpha-2 catalytic chain - fruit N;Alternate names: phosphoprotein phosphatase isoform 87B catalytic chain C;Species: Drosophila melanogaster C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 05-Oct-20(C;Accession: S12960; S05524 R;Dombradi, V.; Axton, J.M.; Barker, H.M.; Cohen, P.T.W. R;Dombradi, V.; Axton, J.M.; Barker, H.M.; Cohen, P.T.W. FEBS Lett. 275, 39-43, 1990
A;Title: Protein phosphatase 1 activity in Drosophila mu A;Reference number: S12960; MUID:91085574; PMID:2175717 Drosophila mutants PMID:2175717 fruit £ly

GB:X55198;

GB:S47852;

NID:98

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A;Cross-references: UNIPARC:UPI000012488F; EMBL:X15583; NID:g8363; PIDN:CAA33609.1; PID:CGenetics:
A;Genetics:
A;Gene: FlyBase:Pp1-87B
A;Cross-references: FlyBase:FBgn0004103
A;Map position: 3R 87B6-12
C;Superfamily: serine/threonine protein phosphatase; phosphoesterase core homology; phosp c;Superfamily: serine/threonine protein phosphoric monoester hydrolase; serine/threonine-species: C;Keywords: iron; metalloprotein; phosphatase homology <PPD>
F;28-287/Domain: phosphoprotein phosphatase homology <PPD>
F;66-284/Domain: phosphoprotein phosphatase homology <PEC>
F;66-284/Domain: phosphopesterase core homology <PEC>
F;62.64.90/Binding site: iron Casp, Asn, His, His, His) #status predicted
F;93,123,270/Active site: Asp, His, Tyr #status predicted
F;93,123,270/Active site: substrate phosphate (Arg) #status predicted
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rosidues: 1-316 <RUN>
A;Rosidues: 1-316 <RUN>
A;Rosidues: 1-316 <RUN>
A;Rosidues: 1-316 <RUN>
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A;Rosidues: 1-316 <RUN
C;Superfamily: serine/threonine protein phosphatase; phosphoesterase core homology <ppp>
C;Roywords: iron; metalloprotein phosphatase homology <ppp>
F;45-303/Domain: phosphoprotein phosphatase homology <ppp>
F;45-303/Domain: phosphoesterase core homology 
F;410-141/Domain: phosphoesterase core homology 
F;73-141/Domain: phosphoesterase core homology 
F;73-141/Domain: phosphoesterase core homology 
F;73-141/Domain: phosphoesterase core homology 
F;107,133,187,262/Binding site: iron (Asp, His, Asp) #status predicted
F;110,140,286/Active site: Asp, His, Tyr #status predicted
F;111,235/Binding site: substrate phosphate (Arg) #status predicted
F;111,235/Binding site: substrate phosphate (Arg) #status predicted
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S26225
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                                                                                                                                                                                                                                                                                                                                                                                                              R;Rundle, S.J.; Nasrallah, J.B.
Plant Mol. Biol. 20, 367-375, 1992
Plant Mol. Biol. 20, 367-375, 1992
A;Title: Molecular characterization of type 1 serine/threonine phosphatases
A;Reference number: S26225; MUID:93043027; PMID:1330067
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A;Title: Cloning and chromosomal localization of Drosophila cDNA encoding A;Reference number: 805524; MUID:89377827; PMID:2550221
A;Accession: S05524
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A; Residues: 1-302 < DOM2>
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FSAPNYCGEFDNAGAMMSIDESLMCSF 307
                           FSASNYYAIGSNKGAYIRLNNQLMPHF 405
                                                      SDP8GDVKGWGANDRGV8YTFGADTVAEFLQKNDMDLICRAHQVVBDGYBFFABRQVVTV
                                                                                  SDPQATMGCVPNTLRGAGVWFGPDVTDNFLQRHRLSYVIRSHBCKPNGHBPMHDNKIITI
                                                                                                               AALID-RILCMHGGISPELMSLDQIRSISR----
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l; Mismatches
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Pred. No. 1.3e-18;
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RESULT 36 Yeast 10, 567-578, ביציא A;Title: The Saccharomyces cerevisiae gene PPH3 encodes a A:Paference number: S44331; MUID:95028155; PMID:7941742 A; Reference number: S44331; A; Accession: S44331 C;Date: 30-Jun-1993 #sequence revision 10-Feb-1995 #text change 05-(C;Accession: 844331; 848762; 855822; 849830; C41525; 867892; 817483 R;Hoffmann, R:, Jung, S:; Ehrmann, M.; Hofer, H.W. Yeast 10, 567-578, 1994 phosphoprotein phosphatase (RC 3.1.3.16) PPH3 - yeast (Saccharomyces N;Alternate names: protein D4421; protein YD8554.08; protein YDR075w C;Species: Saccharomyces cerevisiae A; Molecule type: DNA A; Status: not compared with conceptual translation protein phosphatase cerevisiae) with prope

A;Reference number: S48758 A;Accession: S48762 A;Cross-references: UNIPROT: p32345; UNIPARC: UPI0000053121 R;Coster, F.; Jonniaux, J.L.; Goffeau, A. A; Molecule type: DNA submitted to the EMBL Data Library, A; Residues: 1-308 <HOF> October

A;Residues: 1-308 <COS>
A;Cross-references: UNIPARC:UPI0000053121;
R;Coster, F; Jonniaux, J.L.; Goffeau, A.
Yeast 11, 673-679, 1995
A;Title: Analysis of a 32.8 kb segment of y A; Reference number: 855819; A; Accession: 855822 kb segment of yeast chromosome MUID:96093910; PMID:7483840 ۲ reveals 21

EMBL: X82086; NID: g558241;

PIDN: CAA57602.1;

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A;Molecule type: DNA
A;Residues: 1-308 <COW>
A;Residues: 1-308 <COW>
A;Residues: 1-308 <COW>
A;Cross references: UNIPARC:UPI0000053121; EMBL:X82086; NID:g558241; PIDN:CAA57602.1;
A;Cross references: UNIPARC:UPI0000053121; EMBL:X82086; NID:g558241; PIDN:CAA57602.1;
A;Cross references: UNIPARC:UPI0000053121; EMBL:X82086; NID:g558241; PIDN:CAA57602.1; A;Note: the nucleotide sequence was R;Richards, C.; Harris, D.E. submitted to the EMBL Data Library, A;Reference number: S49823 A;Accession: S49830 A; Status: nucleic acid sequence not shown; translation not November 1994

A;Cross-references: UNIPARC:UPI0000053121; EMBL:Z46796; NID:(R;Ronne, H.; Carlberg, M.; Hu, G.Z.; Nehlin, J.O. Mol. Cell. Biol. 11, 4876-4884, 1991
A;Title: Protein phosphatase 2A in Saccharomyces cerevisiae: A;Reference number: A41525; MUID:92017761; PMID:1656215 A; Molecule type: DNA A; Residues: 1-308 < RIC> NID: g577794; PIDN: CAA86797.1; effects on cell growth PI

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A;Description: phosphoric monoester hydrolase
C;Superfamily: serine/threonine protein phosphatase; phosphoesterase core homology; phos
C;Keywords: iron; metalloprotein; phosphoric monoester hydrolase; serine/threonine-speci
E;17-276/Domain: phosphoprotein phosphatase homology <PPP>
F;45-113/Domain: phosphoprotein phosphatase homology <PEC>
F;45-113/Domain: phosphopsterase core homology <PEC>
F;51,53,79/Binding site: iron (Asp, His, His, His) #status predicted
E;79,111,161,235/Binding site: zinc (Asp, Asn, His, His) #status predicted
F;82,112,259/Active site: Asp, His, Tyr #status predicted
F;83,208/Binding site: substrate phosphate (Arg) #status predicted
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-244,'I',246-308 <RON>
A;Cross-references: UNIPARC:UPI0000168D9C; GB:X58858; NID:g4211; PIDN:CAA41662.1; PID:g4
A;Cross-references: UNIPARC:UPI0000168D9C; GB:X58858; NID:g4211; PIDN:CAA41662.1; PID:g4
A;Cross-references: UNIPARC:UPI0000168D9C; GB:X58858; NID:g4211; PIDN:CAA41662.1; PID:g4
A;Cross-references: UNIPARC:UPI0000168D9C; GB:X58858; NID:g4211; PIDN:CAA41662.1; PID:g4
B;FOUTY, F:; Jonniaux, J.L.; Purnelle, B.; Coster, F.; Goffeau, A.

submitted to the Protein Sequence Database, July 1996
                                                                                                                              A; Molecule type: DNA
A; Residues: 1-33 <DUZ>
A; Cross-references: UNIPROT: P48727; UNIPARC: UPI000013B996;
A; Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                          A; Description: The sequence of A; Reference number: $46729 A; Accession: T16476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphoprotein phosphatase (BC 3.1.3.16) 1-alpha F56C9.1 [similarity] - Caenorhabditis N;Alternate names: protein phosphatase 1, catalytic subunit C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-Oct-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-308 < FOU>
                                                                                                                                                                                                                                                                                                                                                                                              submitted to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: SGD: PPH3; MIPS: YDR075w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S67892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: S67889
;Introns: 18/1; 62/1; 139/1; 210/3; 248/3; 293/3
;Superfamily: serine/threonine protein phosphatase; phosphoesterase core homology; phos
                                                                                                                                                                                                                                                                Status: translated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: T16476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: UNIPARC:UPI000053121; EMBL:Z74371; NID:g1431538; PIDN:CAA98894.1;
                                                                     Gene: CESP:F56C9.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GYKEMFDGGLVTVWSAPNYCYRCGNVAAVLKIDDDLNRBYTIFEAVQAQNE 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNARYGFIREVESKYPRNHKRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NGHEFMHDNKIITIFSASNYYAIGSNKGAYIRLNNQLMPHFVQYISAASQTK 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KTEWQQIFDIMWSDPQ--ATMGCVPNTLRGAGVWFGPDVTDNFLQRHRLSYVIRSHECKP 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RYCCEVFDYLSLGAIINNSIFCVHGGLSPDMTTVDBIRTIDRKQEVP-----HEG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFIDEVYRWLPLGSVLNSRVLIVHGGFS-DSTSLDLIKSIDRGKYVSILRPPLTDGEPLD 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VFRLCLNSQELLMNEGNV-TQVDTPVTICGDIHGQLHDLLTLFEKSGGVEKTR-YIFLGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----AMCDLLWSDPEDVDTWSLSP---RGAGFLFGKREVDQFLEKNNVELIARAHQLVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FVDRGFYSLESFLLLLCYKLRYPDRITLIRGNHETRQITKVYGFYDEVVRKY--GNSNVW
                                                                                                                                                                                                                                                                                                                                                          EMBL Data Library, May 1994 he sequence of C. elegans co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 411.5; DB 1;
Pred. No. 1.3e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 111;
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                                                                                                                                                                   EMBL: U00063; NID: 9488186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25;
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A;Map position: 3

A;Map position: 3

A;Introns: 77/2; 107/2; 145/1; 179/2; 221/3; 265/3; 292/3; 336/1

C;Superfamily: serine/threonine protein phosphatase; phosphoesterase core homology; pho: C;Keywords: iron; metalloprotein; phosphoric monoester hydrolase; serine/threonine-spect P;96-356/Domain: phosphoprotein phosphatase homology <PPP>
F;124-192/Domain: phosphoesterase core homology <PBC>
F;130,132,158/Binding site: iron (Asp, His, Asp) #status predicted P;158,190,240,315/Binding site: zinc (Asp, Asn, His, His) #status predicted P;161,191,339/Active site: Asp, His, Tyr #status predicted F;162,288/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, A;Reference number: Z19166
A;Accession: T19701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphoprotein phosphatase (BC 3.1.3.16) C34C12.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 05-Oct-2004 C;Accession: T19701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Keywords: glycogen metabolism; heterodimer; iron; metalloprotein; phosphoric monoeste. F;29-288/Domain: phosphoprotein phosphatase homology <PPP>
F;57-125/Domain: phosphoesterase core homology <PPC>
F;63,65,91/Binding site: iron (Asp, His, Asp) #status predicted
F;91,123,172,247/Binding site: zinc (Asp, Asn, His, His) #status predicted
F;94,124,271/Active site: Asp, His, Tyr #status predicted
F;95,220/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPARC:UPI0000172815; A;Experimental source: clone C34C12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: translated from A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Kershaw,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
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Best Local :
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          117
                                                      141 NISPVSTAVSQQVTVCGDLHGKLDDLLVVLHKNGLPSSSNPYVFNGDFVDRGKRGLEVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          394 YIRLMNOLMPHFVQYISAASQTK 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       275 S-DSTSLDLIKSIDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMGCVPNTLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215 LNRGNHEDSVMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155 VCGDLHGKLDDLLVVLHKNGLPSSSNPYVFNGDFVDRGKRGLEVLLLLLLSLYLAFPNAVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 LPIRKNHIDLLIDVFRKKRGNRLHPKYVALI---LREAAKSLKQLPNISPVSTAVSQQVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDVEKLNLÖNIISRLLEVRÖSK-PGKNVQLTESEIKGLCQKSREIFLSQPILLELEAPLK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1-382 <WIL>
                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MMTVDETLMCSF-QILKPADKKK
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                                                                                                          Conservative
PVTICGDIHGQFYDLL-BLFKTGGTVPNTKYVFMGDYVDRGHYSLBTVT
                                                                                                                                 11.9%;
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                                                                                                          45;
                                                                                                                                 Score 409.5; DB 1;
Pred. No. 2.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 411.5; DB 1;
Pred. No. 1.5e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     December
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL: Z46996; PIDN: CAA87100.1; GSPDB: GN00021;
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                                                                                                          Indels
                                                                                                                                                        Length
                                                                                                          25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25;
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                                                                                                       Gaps
            171
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R;Smith, R.D.; Walker, J.C.

R;Smith, R.D.; Walker, J.C.

R;Smith, R.D.; Walker, J.C.

R;Smith, R.D.; Walker, J.C.

R;Description: Isolation and expression of maize type 1 protein phosphatase.

A;Reference number: S29317

A;Reference number: S29317

A;Reference sumber: S29317

A;Reledule type: mRNA

A;Residuse: 1-316 <SMI>
A;Residuse: 1-316 <SMI>
A;Cross-references: UNIPROT:P22198; UNIPARC:UPI0000131FBD; EMBL:M60215; NID:g168722; PIE
C;Superfamily: serine/threonine protein phosphatase; phosphoesterase core homology; phosphorics: iron; metalloprotein; phosphoric monoester hydrolase; serine/threonine-specif;27-286/Domain: phosphoprotein phosphatase homology <PPP>
F;61,63,89/Binding site: iron (Asp. His, Asp.) #status predicted
F;89,121,170,245/Binding site: asp, His, Tyr #status predicted
F;93,218/Binding site: substrate phosphate (Arg) #status predicted
F;93,218/Binding site: substrate phosphate (Arg) #status predicted
RESULT 40
S31089
phosphoprotein phosphatase
N;Alternate names: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 39
S29317
S29317
phosphoprotein phosphatase (EC 3.1.3.16) 1 - maize C/Species: Zea mays (maize)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995
C/Accession: S29317
R/Smith, R.D.; Walker, J.C.
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    (EC 3.1.3.16)
T6H20.150
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Pred. No. 2e-18;
                       1 catalytic chain
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A;Cross-references: UNIDARC:UPI0000131PB5; EMBL:AL096859; GSPDB:GN00061; ATSP:T6H20.150
A;Experimental source: Cultivar Columbia; BAC clone T6H20
C;Genetics:
A;Gene: ATSP:T6H20.150
A;Map position: 3
A;Introns: 69/1; 255/3
A;Introns: 69/1; 255/3
C;Superfamily: serine/threonine protein phosphatase; phosphoesterase core homology; phos
C;Keywords: iron; metalloprotein; phosphatase homology <a href="https://documbia.com/protein/phosphatase/monoester/pypp-">https://documbia.com/pypp-</a>
C;Keywords: iron; metalloprotein phosphatase homology <a href="https://documbia.com/phosphoprotein/phosphatase/monology">https://documbia.com/phosphoprotein/phosphatase/monology</a> <a href="https://documbia.com/phosphoprotein/phosphatase/monology">https://documbia.com/phosphoprotein/phosphatase/monology</a> <a href="https://documbia.com/phosphoprotein/phosphatase/monology">https://documbia.com/phosphoprotein/phosphatase/monology</a> <a href="https://documbia.com/phosphatase/monology">https://documbia.com/phosphoprotein/phosphatase/monology</a> <a href="https://documbia.com/phosphatase/monology">https://documbia.com/phosphoprotein/phosphatase/monology</a> <a href="https://documbia.com/phosphatase/monology">https://documbia.com/phosphoprotein/phosphatase/monology</a> <a href="https://documbia.com/phosphatase/monology">https://documbia.com/phosphoprotein/phosphatase/monology</a> <a href="https://documbia.com/phosphatase/monology">https://documbia.com/phosphoprotein/phosphoprotein/phosphatase/monology</a> <a href="https://documbia.com/phosphatase/monology">https://documbia.com/phosphoprotein/phosphatase/monology</a> <a href="https://documbia.com/phosphatase/monology">https://documbia.com/phosphatase/monology</a> <a href="https://documbia.com/phosphatase/monology">https://documbia.com/phosphatase/monology</a> <a href="https://documbia.com/phosphatase/monology">https://documbia.com/phosphatase/monology</a> <a href="https://documbia.com/phosphatase/monology">https://documbia.com/phosphatase/monology</a> <a href="https://documbia.com/phosph
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S31089; T19966
R;Smith, R.D.; Walker, J.C.
Plant Mol. Biol. 21, 307-316, 1993
A;Title: Expression of multiple type 1 phosphoprotein phosphatases in Arabidopsis thalic A;Reference number: S31085; MUID:93144705; PMID:7678768
A;Reference number: S31089
A;Reference number: S31089
A;Reference number: S31089
A;Accession: S31089
A;Accession: S1089
A;Rolecule type: mRNA
A;Residues: 1-312 <SMI>A;Cross-references: UNIPROT:P48485; UNIPARC:UPI0000131FB5; EMBL:M93412; NID:g166802; PIL R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sasubmitted to the Protein Sequence Database, July 1999
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A;Accession: T12966
A;Molecule type: DNA
A;Residues: 1-312 <CHO>
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Search completed: January 20, 2006, 19:52:41 Job time: 42 secs

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Result
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2: uniprot_trembl:*
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Copyright (c) 1993 - 2006 Compugen Ltd.
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Q4GP57 TETING
Q4Y018 PLACH
Q81728 TRYCR
Q512P5 ENTHI
Q9188 CAEEL
Q4Z5E3 PLABE
Q8WR3 PLAPA
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Q8VH81 DROME
Q55UAB CRYHO
Q9VH81 DROME
Q55UAB CRYHO
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Q4ggm70

Q4ggm71

Q4rft2

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Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

# M. G.	uri V., F	Pan S.,	ເດ. ເວ	M., Pittman	Palazzolo M.,		
D.L.,	Muzny D.M., Nelson	B., Murphy L	hdri		fount S.M.,		
	o., McPherson D.	Mobarry C.,	i B., McIntosh Milshina N.V.,	` [6]	രൂ.		
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ĕin D.	s-Pfannkoch C., ktaroglu L., Bea	. : :	В:,	mio	Abril J.F., F Ballew R.M.,		
klos G.L.G.,	, Pfe	C., Blazej R.G. E.G., Helt G.,	Rogers YH.C., B e C., Baxter E.G.	2	Brandon R. Wan K.H.,		
S	O O	Richards S., Ash, Yandell M.D.,	В., J.R.	:: ≠∺	George R.A. Sutton G.G.		
٦.	Hoskins R.A., Galle R.	; 5	rer	Celni P.G.,	Adams M.D., Amanatides		
61.2185;	126/science.287.5	, DOI =	PubMed=10731132;		MEDLINE 20196006		
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	encodes	age (;	retinal degeneration nine protein phosphat	a retin	"Drosophila retina serine/threonine p		
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		ophilidae, Drosophila.	ea; Drosophilidae; D=7227;	a; Dros =7227;	ydroid I_TaxI	22	
	Insecta; Pterygota;	poda; Hexapoda; intera: Brachyc	a; Arthro	Metazoa;	Bukaryota; Neoptera:		
		; ruit fly).	es=CG6571 qaster (F	ORFNam melano	Name=rdgC; ORFNames=CG65 Drosophila melanogaster		
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•	е)	annotation upo	48, Last	)5 (Rel.	3-SEP-200		
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GO; GO:0005516; F:calmodulin

GO; GO:0019722; P:calcium-me

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GO; GO:0007602; P:phototrans

GO; GO:0006470; P:protein and

InterPro; IPR011992; BF-Hand

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Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
--- **TMCTTON: Phosphatase required to prevent light-induced retinal
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MEDLINE=22426069, PubMed=12537572;

Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.

Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Berman B.

Bettencourt B.R., Celniker S.B., de Grey A.D.N.J., Drydaale R.A.,

Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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                                                                                                                                InterPro; IPR011992; EP-Hand type.
InterPro; IPR012048; EF hand Ca bd.
InterPro; IPR002048; IQ-Cam bd_region.
InterPro; IPR004843; M-pesterase.
InterPro; IPR012008; PPEF.
InterPro; IPR012008; PPEF.
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GO:0019722; P:calcium-mediated signaling; TAS.
GO:0016059; P:deactivation of rhodopsin mediated signaling;
GO:0007602; P:phototransduction; IMP.
GO:0006470; P:protein amino acid dephosphorylation; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=P40421-2; Sequence=VSP_009324;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Expressed in the visual systems of
well as in the mushroom bodies of the central brain.
SIMILARITY: Belongs to the PPP phosphatase family.
SIMILARITY: Contains 3 BF-hand domains.
SIMILARITY: Contains 1 IQ domain.
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COPACTOR: Binds 1 manganese ion
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ALIERNATIVE PRODUCTS:
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; Q08209; 1AUI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M89628; AAB00734.1; -; Genomic DNA.
AE003514; AAF49044.2; -; Genomic DNA.
AE003514; AAO41217.1; -; Genomic DNA.
                                          PF00036; efhand; 3.
PF00612; IQ; 1.
PF00149; Metallophos; 1.
PIRSF000912; PPEF; 1.
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IsoId=P40421-1; Sequence=Displayed;
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Alternative splicing; Calcium; Hydrolase;
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                         HRKEQQDENIRRRSTGRPSVÅKTATDPVTLLADKISKNTLVVEHDIDPTDCESKVIDPKK
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Manganese (By similarity).
Manganese (By similarity).
Missing (in isoform A).
/FTId=VSP 009124.
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EF-hand
EF-hand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 3442; DB 1
Pred. No. 2e-200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proton
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         donor (By similarity).
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Best Local S
Matches 602
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A Park S., Wan K., Yu C., Rubin G.M., Celniker S.;
L Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
R EMBL, BT01.5959; ANJ8644.1; -; mRNA.
GO; GO:0005509; F:calcium ion binding; IEA.
R GO; GO:0016787; F:hydrolase activity; IEA.
R GO; GO:0016787; F:hydrolase activity; IEA.
R InterPro; IPR002048; BF-hand.
R InterPro; IPR006186; T-phtase_apaH.
R InterPro; IPR006186; T-phtase_apaH.
R Ffam; pF00036; efhand; 3.
R Pfam; pF00036; eFhand; 3.
R Pfam; pF000149; Metallophos; 1.
R PRINTS; RR00114; STPHPHTASE.
R PRODOm; PD000012; BF-hand; 1.
R ProDom; PD000012; BF-hand; 1.
R PRODOm; PD000012; BF-hand; 1.
R PROSITE; PS00018; BF HAND; UNKNOWN 2.
R PROSITE; PS00125; SER THR PHOSPHATASE; UNKNOWN 1.
R PROSITE; PS00125; SER THR PHOSPHATASE; UNKNOWN 1.
R PROSITE; PS00125; SER THR PHOSPHATASE; UNKNOWN 1.
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01-FEB-2005
01-FEB-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LT 2
D3 DROMB
Q5U1D3 I
Q5U1D3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
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                                                                                                    241
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                  419
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                                                                                                                                                                                                                                                                                                                                                                                              602;
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                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                           YPRWHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGFSDSTSLDLIKSIDRGKYVSILRPP
                                                                                                                                                                                                                                    SNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNARYGFIREVESK
                                                                                                                                                                                                                                                                                                                                                 MPQAAGRKNQYQGSAHVSVLDDKDDLVEEFGDIVNAKIELPIRKNHIDLLIDVFRKKRGN
SFKQRMGIVESSALKELAVRMRDHRDELEDEFRKYDPKDSGYISISHWCKVMENVTKLGL
                                                             SHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRLNNQLMPHFVQYISAASQTKRL
                                                                                                                     LTDGEPLDKTEWQQIFDIMWSDPQATMGCVPNTLRGAGVWFGPDVTDNFLQRHRLSYVIR
                                                                                                                                                                                                                   SNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNARYGFIREVESK
                                                                                                                                                                                                                                                                           RLHPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLLVVLHKNGLPSS
                                                                                                                                                                                                                                                                                             RLHPKYVALITLREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLLVVLHKNGLPSS
                                                                                                                                                                                                                                                                                                                                    MPQAAGRKNQYQGSAHVSVLDDKDDLVEEFGDIVNAKIELPIRKNHIDLLIDVFRKKRGN
                                                                                                                                                            YPRNHKRILAFIDBVYRWLPLGSVLNSRVLIVHGGFSDSTSLDLIKSIDRGKYVSILRPP
                                                                                                   LTDGEPLDKTEWQQIFDIMWSDPQATMGCVPNTLRGAGVWFGPDVTDNFLQRHRLSYVIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 661
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 29, Created)
(TrEMBLrel. 29, Last sequence update)
(TrEMBLrel. 29, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                         90.7%;
                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                           Score 3121; DB 2;
Pred. No. 5.3e-181;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
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                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                  478
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RESULT 3
Q70229 ANOGA
Q70229 ANOGA PRELIMINARY;
PR
Q70229;
AC
Q70229;
DT
O1-MAR-2004 (TrEMBLrel. 26, Last
DT
O1-MAR-2004 (TrEMBLrel. 26, Last
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O1-MAR-2004 (TrEMBLrel. 26, Last
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O1-MAR-2004 (TrEMBLrel. 26, Last
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O1-MAR-2004 (TrEMBLrel. 26, Last
DT
O2 Anopheles gambiae str PEGT.
O2 Anopheles EST;
CAMPIANI-PEST;
CAMP
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  Query Match
Best Local Sin
Matches 366;
                                                                                                                                                                                                                                                                   ProDom; PD000012; EF-hand; 1.
ProDom; PD000252; T phtase apaH;
SMART; SM00054; EFh; 2.
SMART; SM00156; PPZAC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AAAB01008966; EAA12933.2; -; Genomic DNA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR002048; EF-hand.
InterPro; IPR000048; IQ region.
InterPro; IPR004843; M-pesterase.
InterPro; IPR004843; M-pesterase.
InterPro; IPR006186; T_bhtase_apaH.
PF00036; efhand; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Anopheles gambiae Sequence Committee, "Anopheles gambiae re-annotation."; Submitted (APR-2002) to the EMBL/GenBank,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anopheles gambiae str. PEST
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neoptera; Endopterygota; Diptera; Anophelinae; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAUTION: The sequence shown here is derived EMBL/GenBank/DDBJ whole genome shotgun (WGS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               599
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                                 Similarity
                                                                                                                                                                          PS00018; EF_HAND; UNKNOWN_2.
PS50096; IQ; 1.
PS00125; SER_THR_PHOSPHATASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
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                              56.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence Committee;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the EMBL/GenBank/DDBJ databases
%; Score 1930.5;
k; Pred. No. 1e-1
101; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                            BAOAAEAFEF89D548
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                                                                                                                                                                                     UNKNOWN_1.
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                                                       DB 2; Length
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                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    From
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                                                          613;
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Conservative

130;

Indels

17;

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RESULT ON THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL
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QTQNIO;
QTQNIO;
Q1-MAR-2004 (TrEMBLrel. 26, Created)
Q1-MAR-2004 (TrEMBLrel. 26, Last sequence update)
Q1-MAR-2004 (TrEMBLrel. 26, Last sequence update)
Q1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ENSANGPO00000059 (Fragment).
QRENAMGPESUSANGG000000057;
QRENAMGPESUSANGG00000057;
Anopheles gambiae str. PEST.
ENKATYOTA; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Neoptera; Anopheles.
                                                         STRAIN=PEST;
The Anopheles gambiae Se
Submitted (APR-2004) to
                                                                                                                                                              The Anopheles gambiae Sequence Committee; "Anopheles gambiae re-annotation."; Submitted (APR-2002) to the EMBL/GenBank/
                                                                                                                                                                                                                                                              NCBI_TaxID=180454;
[1]
                                                                                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANOGA
                    Anopheles gambiae Sequence Committee;
mitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry v
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ProDom; PD000252; T_phtase_apaH; 1.

SMART; SM00054; EFh; 2.

SMART; SM00054; EP; 2.

SMART; SM00156; PP2Ac; 1.

PROSITE; PS00018; EF HAND; UNKNOWN_2.

PROSITE; PS00096; IQ; 1.

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InterPro; IPR000048; IQ region.
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RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Micaud S., Jaffe D., Fishers S., Lutfalla G., Dossat C., Segurens B.,
RA Micaud S., Jaffe D., Fishers S., Lutfalla G., Dossat C., Segurens B.,
RA Anthouard V., Jubin C., Cattelli V., Katinka M., Vacherie B.,
RA Anthouard V., Jubin C., Cattelli V., Katinka M., Vacherie B.,
RA Anthouard V., Jubin C., Cattelli V., Katinka M., Vacherie B.,
RA Anthouard V., Skalli Z., Cattelli V., Katinka M., Vacherie B.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Wincker P., Lander E.S., Weissenbach J., Roset Crollius H.,
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
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Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Euteleostei; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontoidea; Tetraodontidae; Tetraodon.
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13-SEP-2005 (TrEMBLrel. 31, Last sequ
13-SEP-2005 (TrEMBLrel. 31, Last anno
Chromosome 4 SCAF14533, whole genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preliminary data.
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capacitation (CAAB01014533; CAF97171.1; -; Genomic_
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                                                                                                                 LDAIARVDRHKYVSALRPPKLKNQAANEKRAGAAGPMEGRRRVYTLTYKSTAADHSHKRP
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(FEB-2004) to
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81541 MW;
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Pred. No. 1e-74,
7; Mismatches 1
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                                                                               MEDLINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RX Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschal S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschal S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Warusina K., Famer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Westernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human
"Generation and initial analysis of more than 15,000 full-length human
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Muroidea; Muridae;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nathans J.;
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MEDLINE=97471020;
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13-SEP-2005
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                                    mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A.
         FUNCTION:
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(Rel. 40, Last sec
(Rel. 48, Last and
   May play a role
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Sun H., Macke J.P.,
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48, Last annotation update)
protein phosphatase with EF-hands-2
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                                    99:16899-16903 (2002) .
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   in phototransduction.
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Rodentia; Sciurogna
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SMART; SM00156; PP2AC; 1.

PROSITE; PS00018; EF HAND 1; 3.

PROSITE; PS0022; EF HAND 2; 3.

PROSITE; PS0026; IQ; 1.

PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.
                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0114; STPHPHTASE.
ProDom; PD000012; Er-hand; 1.
ProDom; PD000252; T_phtase_apaH;
SMART; SM00054; EFh; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR011992; EF-Hand_type.
InterPro; IPR002048; EF hand_Ca_bd.
InterPro; IPR000048; IO_CaM_bd_region.
InterPro; IPR004843; M_pesterase.
InterPro; IPR012008; PPEF.
InterPro; IPR006186; T_phtase_apaH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF023458;
EMBL; BC027049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGI; MGI:1342304; Ppef2.
                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                       Calcium; Hydrolase; Iron; Manganese; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                   PIRSF; PIRSF000912; PPEF;
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SIMILARITY: Contains 3 BF-hand do
SIMILARITY: Contains 1 IQ domain.
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SIMILARITY: Bel
SIMILARITY: Cor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COFACTOR: Binds 1 manganese ion ENZYME REGULATION: Activated by TISSUE SPECIFICITY: Detected in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphate.
COFACTOR: Binds 1 iron ion
COFACTOR: Binds 1 manganese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dephosphorylate photoactivated rhodopsin. May function as a calcium sensing regulator of ionic currents, energy product; synaptic transmission.

CATALYTIC ACTIVITY: A phosphoprotein + H(2)0 = a protein +
                                                                                                                                                                                                                                                                                                                                                                                        PF00036; efhand; 3.
PF00612; IQ; 1.
PF00149; Metallophos; 1.
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                                                                               Similarity
                                                                                                                                                                                                                                                               phosphatase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ENSMUSG00000029410; Mus musculus
EKAFKAAALIQRWYRRYMARLEMRRRCTWNIFQSIEYAGQQDQVKLHEFFSYLVDHFTPS
                                                                    39.5%;
illarity 38.9%;
Conservative 11:
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AAH27049.1; -; mRNA.
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                                                                                                                                                                                                                                                            transduction; Vision
                                                                              5e-74;
                                                                                         DB 1;
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                                     InterPro;
InterPro;
InterPro;
                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.

The C.briggsae Sequencing Consortium;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ dat
-!- CAUTION: The sequence shown here is derived f
EMBL/GenBank/DDBJ whole genome shotgun (WGS)
                                                                                                 InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis briggsae.
Bukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical | Name=CBG15166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q616S0 CAEBR PRELIMINARY;
                                     O; GO:0005509; F:calcium ion binding; II
O; GO:0016787; F:hydrolase activity; IE
nterPro; IPR002048; EF-hand.
nterPro; IPR000048; IQ_region.
nterPro; IPR004843; M-pesterase.
nterPro; IPR012008; PPEF;
nterPro; IPR0126186; T_phtase_apaH.
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PF00036; efhand; PF00612; IQ; 1.
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(TIEMBLrel. 28, Last sequence update)
(TIEMBLrel. 28, Last annotation update)
protein CBG15166.
                T_phtase_apaH.
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RESULT 8
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Best Local S
Matches 269
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PIRSP; PIRSP00912; PPEF; 1.
PRINTS; PR00114; STPHPTASE;
PRODOm; PD000012; EF-hand; 1.
PRODOm; PD000252; T_Dhtase_apaH; 1
SWART; SM00054; EFh; 2.
SMART; SM00156; PP2Ac; 1.
                                                    PPE2 HUMAN S
014830; 014831;
16-OCT-2001 (Rel
16-OCT-2001 (Rel
13-SEP-2005 (Rel
Homo sapiens (Human)
Eukaryota; Metazoa;
                      Name=PPEF2;
                                           Serine/threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
SEQUENCE 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00018; EF HAND; UNKNOWN 2.
PROSITE; PS00125; SER THR_PHOSPHATASE; UNKNOWN 1.
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                                                                                                                                                     TDYIAQIAES---IDFNKDGFIDLNELLEAFRLVD
                                                                                                                                                                      ----AEMLEKCRMMDLNGDGKVDLNEFLEAFRLSD
                                                                                                                                                                                                                        AEADGMSVMDALYANKASLVAIFNIIDADNSGEITLDEFETAIDLLVAHMPGAYSK----
                                                                                                                                                                                                                                             DLEKSGNLPILKWSECVERITGLNLPWIALAPKVATLSDDGKFVNYKEDRKIAQVGGTHA
                                                                                                                                                                                                                                                                 DPKDSGYISISHWCKVMENVTKLGLPWRLLRDKLAPGTDSQK-VNYNRTLDLLDTDVILB
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                                                                                                                                                                                                   QEKD---IVESLYRHKSTLETLFRFMDKDNSGQVSMKEFIDACEVL----
                                                   (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 48, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative 118;
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                                                                                                  STANDARD;
                                          protein
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Chordata;
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                                          phosphatase with
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Pred. No. 7
Craniata;
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                                                                                                 753
                                                     update)
Vertebrata;
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                                           EF-hands-2
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Euteleostomi;
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Pfam; PP00036; efhand; 3.

Pfam; PP00016; IQ; 1.

Pfam; PP00149; Metallophos; 1.

Pfam; PP00149; Metallophos; 1.

PIRSF; PIRSF000912; PPEF; 1.

PRINTS; PR00114; STPHPHTASE.

PRODOm; PD000012; EF-hand; 1.

PRODOm; PD000052; Tphtase apaH; 1.

PRODOm; PD000054; EFh; 3.

SMART; SM00015; IQ; 1.

SMART; SM0015; IQ; 1.

SMART; SM0016; PP2Ac; 1.

PROSITE; PS00018; EF HAND 1; 2.

PROSITE; PS00016; IQ; PALSE NEG.

PROSITE; PS0096; IQ; PALSE NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0004722; F:protein serine/threonine phosphatase activity; GO:0006470; P:protein amino acid dephosphorylation; TAS. InterPro; IPR011992; EF-Hand_type. InterPro; IPR002048; EF hand_Ca_bd. InterPro; IPR000048; IQ_CAM_bd_region. InterPro; IPR004048; M-pesterase. InterPro; IPR004083; M-pesterase. InterPro; IPR004083; M-pesterase. InterPro; IPR00408; PBF. InterPro; IPR006186; T_phtase_apaH. Pfam; PP00036; efhand; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF023456; AAB82796.1; -; EMBL; AF023457; AAB82797.1; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This Swiss-Prot entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use as long as its content is in no way modified and this statement is no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97471020; PubMed=9326663; Sherman P.M., Sun H., Macke J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             serine/threonine
degeneration C.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ensembl; ENSG00000156194; Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 removed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification and characterization of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=014830-2; Sequence=VSP_005103, TISSUE SPECIFICITY: Retinal specific SIMILARITY: Belongs to the PPP phospha: SIMILARITY: Contains 3 EP-hand domains SIMILARITY: Contains 1 IQ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphate.

COPACTOR: Binds 1 iron ion per subunit (By similarity).

COPACTOR: Binds 1 manganese ion per subunit (By similar COPACTOR: Binds 1 manganese ion per subunit (By similarity).

ENZYMB REGULATION: Activated by calcium (By similarity).

SUBCELLULAR LOCATION: Localized to photoreceptors, PPEF least 2 fold more abundant in rod inner segments than i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     synaptic transmission.
CATALYTIC ACTIVITY: A phosphoprotein + H(2)0 = a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        c. Natl. Acad. Sci. U.S.A. 94:11639-11644(1997).
FUNCTION: May play a role in phototransduction. May dephosphorylate photoactivated rhodopsin. May function as a calcium sensing regulator of ionic currents, energy production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bvent=Alternative
Name=PPEF-2(L);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   segments.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=PPBF-2(S);
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                     PS00018; EF_HAND_1; 2.
PS50222; EF_HAND_2; 3.
PS50026; IQ; FALSE NG:
PS00125; SER_THR_PHOSPHATASE; 1.
PS00125; SER_THR_PHOSPHATASE; 1.
ive splicing; Calcium; Hydrolase;
nding; Polymorphism; Protein phosp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Vision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphatase family.
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AIFNIIDADNSGEITLDEFETAIDLLVAHMPGAYSKAEMLEKC-----RMMDLNGDGKVD
                                            VTKLGLPWRLLRDKLAPGTDSQKVNYNRTLDLLDTDVILEAEADGMSVMDALYANKASLV
                                                                   KVTHTLTMRQRISRVEBSALRALREKLFAHSSDLLSEFKKHDADKVGLITLSDWAAAVES
                                                                                      SQTKRLSFKQRMGIVESSALKELAVRMRDHRDELEDEFRKYDPKDSGYISISHWCKVMEN
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38.1%;
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Manganese (By similarity).
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OCISAL_CAREL PRELIMINARY; PRT; 707 AA.

OCISAL_CAREL PRELIMINARY; PRT; 707 AA.

OCISAL_CAREL PRELIMINARY; PRT; 707 AA.

OCISAL_CAREL PRELIMINARY; PRT; 707 AA.

OCISAL_CAREL PRELIMINARY; PRT; 707 AA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Identification and characterization of a conserved family of protein serine/threonine phosphatases homologous to Drosophila retinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     659
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  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=9326663; DOI=10.1073/pnas.94.21.11639; H., Macke J.P., Williams J., Smallwood P.M.,
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JARAYO MACFA PRELIMANCE.

ID QARAYO MACFA PRELIMANCE.

AC QARAYO;

DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLerel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLerel. 31, Last annotation update)

DE Brain cDNA, clone: QtrA-11374, similar to human protein phosphatase,

DE EP hand calcium-binding domain 1(PPEFI), transcript variant 1,.

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

OC Mammalia; Craniate; Cercopithecinae; Macaca.
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Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y., Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.; "Substitution rate and structural divergence of 5'0TR evolution: Comparative analysis between human and cynomolgus monkey cDNAs." Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                   International consortium for macaque cDNA "DNA sequences of macaque genes expressed evolutionary implications.";
Submitted (JUN-2005) to the EMBL/GenBank/I
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PRESULT 11

PPEI HUMAN

ID PREI HUMAN

O14829; O15253; Q9NU21; Q9UJHO;

AC O14829; O15253; Q9NU21; Q9UJHO;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2005 (Rel. 40, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Serine/threonine protein phosphatase with EP-hands-1 (EC 3.1.3.16)

DE (PPEP-1) (Protein phosphatase with EP-hands-1 (EC 3.1.3.16)

DE (Serine/threonine protein phosphatase 7) (PPT)

DE (Serine/threonine protein phosphatase 7)

OC Serine/threonine protein phosphatase 7)

ON Name-PPEP1; Synonyms=PPEP, PPP7C;

GN Name-PPEP1; Synonyms=PPEP, PPP7C;

ON Name-PPEP1; Synonyms=PPEP, PPP7C;

ON Name-PPEP1; Synonyms=PPEP, PPP7C;

OC Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

OC Homo.

ON NCBI TaxID=9606;

RN [1]

RR NUCLEOTIDE SEQUENCE.

TISSUE=Retina;

RX MEDLINE=97471020; PubMed=9326663; DOI=10.1073/pnas.94.21.11639;

RA Sherman P.M., Sun H., Macke J.P., Williams J., Smallwood P.M.,

RA Nathans J.;
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RR Ross M.T., Grafham D.V., Coffey A.J., Scherer S., McLay K., Muzny D.,
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RA Lovell F.L., Howe K.L., Abhurst J.L., Fulton R.S., Sudbrak R., Wen G.,
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RA Hunt P.J., Hunt A.R., Isherwood J., Johnson D., Jones S.,
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RA Hunt P.J., Hunt A.R., Isherwood J., Jacob L., Johnson D., Jones S.,
RA Ciccodica P., Klages S., Krights A., Korlara G
      Wall M., W
Whitehead
Williams G
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PubMed=9215685; DOI=10.1093/hmg/6.7.1137; Montini B., Rugarli E.I., van de Vosse E., Andolfi G., Mariani M., Puca A.A., Consales G.G., den Dunnen J.T., Ballabio A., Franco B.; Paca A.A., Consales G.G., den Dunnen J.T., Ballabio A., Franco B.; Paca A.A., Consales G.G., den Dunnen J.T., Ballabio A., Franco B.; Paca A.A., Consales G.G., den Dunnen J.T., Ballabio A., Franco B.; Paca A.A., Consales G.G., den Dunnen J.T., Ballabio A., Franco B.; Paca A.A., Consales G.G., den Dunnen J.T., Ballabio A., Franco B.; Paca A.A., Consales G.G., den Dunnen J.T., Ballabio A., Franco B.; Paca A.A., Consales G.G., den Dunnen J.T., Ballabio A., Franco B.; Paca A.A., Consales G.G., den Dunnen J.T., Ballabio A., Franco B.; Paca A.A., Consales G.G., den Dunnen J.T., Ballabio A., Franco B.; Paca A.A., Consales G.G., den Dunnen J.T., Ballabio A., Franco B.; Paca A.A., Consales G.G., den Dunnen J.T., Ballabio A., Franco B.; Paca A.A., Consales G.G., den Dunnen J.T., Ballabio A., Franco B.; Paca A.A., Consales G.G., den Dunnen J.T., Ballabio A., Franco B.; Paca A.A., Consales G.G., den Dunnen J.T., Ballabio A., Franco B.; Paca A.A., Consales G.G., den Dunnen J.T., Ballabio A., Franco B.; Paca A.A., Consales G.G., den Dunnen J.T., Ballabio A., Franco B.; Paca A.A., Consales G.G., den Dunnen J.T., Ballabio A., Franco B.; Paca A.A., Consales G.G., den Dunnen J.T., Ballabio A., Franco B.; Paca A.A., Consales G.G., den Dunnen J.T., Ballabio A., Paca A.A., Consales G.G., den Dunnen J.T., Ballabio A., Paca A.A., Consales G.G., den Dunnen J.T., Ballabio A., Paca A.A., Consales G.G., den Dunnen J.T., Ballabio A., Paca A.A., Consales G.G., den Dunnen J.T., Ballabio A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A., Paca A
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TISSUE=Fetal brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPLICE ISOFORM(S) THAT ARE POTENTIAL NMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22388257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphate.

COPACTOR: Binds 1 iron ion per subunit (By s
COPACTOR: Binds 1 manganese ion per subunit
COPACTOR: Magnesium (By similarity).

ENZYME REGULATION: Activated by calcium.
BIOPHYSICOCHEMICAL PROPERTIES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Optimum pH is 8.0;
ALTERNATIVE PRODUCTS:
Event=Alternative eplicing; Named isoforms=5;
                                                                                 retinoblastoma cells. Also found in fetal brain. SIMILARITY: Belongs to the PPP phosphatase famil SIMILARITY: Contains 3 EF-hand domains. SIMILARITY: Contains 1 IQ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of photoreceptors. May have a role in c
CATALYTIC ACTIVITY: A phosphoprotein +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: May have a role in the recovery or adaptation response of photoreceptors. May have a role in development.
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                                         Swiss-Prot
                                                                                                                                                                                                                                                                IsoId=014829-4; Sequence=VSP 005100, VSP 005101; Note=May be produced at very low levels due to a codon in the mRNA, leading to nonsense-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Natl. Acad.
                                                                                                                                                                                                 Note=May have no functional significance;
                                                                                                                                                                                                                                                                                                                                                          IsoId=014829-3;
                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=014829-2;
                                                                                                                                                                                                                          IsoId=014829-5; Sequence=VSP_005102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=014829-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dependence:
                                                                                                                                                                         SPECIFICITY: Detected in retina and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE [LARGE SCALE MRNA]
                    rot entry is copyright. It is produced through Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5:RESEARCH008.1-RESEARCH008.16(2004)
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                                                                                                                                                                                                                                                                                                                                                      Sequence=VSP_005099
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence=VSP_005098
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence=Displayed,
                                                                                                                                                                                                                                                                    low levels due to a premature nonsense-mediated mRNA decay
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                                                                                                                                                                              derived
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Bioinformatics Institute.

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EMBL outstation

removed.

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MIM;

547

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RGO; GO:0004722; F:protein serine/threonine phosphatase activity; TAS.

GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.

RINTERPO; IPRO11992; EF-Hand_type.

RINTERPO; IPRO02048; EF-Hand_Ca_bd.

RINTERPO; IPRO02048; EF-Hand_Ca_bd.

RINTERPO; IPRO04843; M-pesterase.

RINTERPO; IPRO04843; M-pesterase.

RINTERPO; IPRO06186; T_phtase_apaH.

Pfam; PF00036; efhand; 3.

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Best Local Similarity 40.3%;
Matches 258; Conservative 12
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MIM; 300109; -.
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3L; X97867; CAA86461.1; -; mRNA.
3L; AF027977; AAC05825.1; -; mRNA.
3L; AL0967700; CA142857.1; -; Genomic_DNA.
3L; Z94056; CA142857.1; JOINED; Genomic_DNA.
3L; Z94056; CA142777.1; -; Genomic_DNA.
3L; Z94056; CA142777.1; JOINED; Genomic_DNA.
3L; AL0967700; CA142777.1; JOINED; Genomic_DNA.
3L; BL096700; CA142777.1; JOINED; Genomic_DNA.
3L; BC036026; AAH36026.1; -; mRNA.
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   LEDEFRKYDPKDSGYISISHWCKVWENVTKLGLFWRLLKDKLAPGTDSQKVNYNRTLDLL
                                                                                                                                                           SNKGAYIRLNNQLMPHFVQYISAASQTKRLSF---KQRMGIVESSALKELAVRMRDHRDE
                                                                                                                                                                                                                                                                                                                           PNTLRGAGVWFGFDVTDNFLQRHRLSYVIRSHECKFNGHEFMHDNKIITIFSASNYYAIG
                                                                                                                                                                                                                                                                                                                                                                                                                      PL-----TDGEP---LDKTEWQQIFDIMWSDPQATMGCV
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                                                                                                                                                                                                                                                                       PNTCRGGGCYFGPDVTSKILNKYQLKMLIRSHECKPEGYEICHDGKVVTIFSASNYYEEG
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                                                                                                                       ----QVTKATCFQPLRQRVDTMENSAIKILRERVISRKSD
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Matches 260
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R InterPro; IPR002048; BF-hand.
R InterPro; IPR0011992; BF-Hand_type.
R InterPro; IPR000484; IQ region.
R InterPro; IPR004843; M-pesterase.
R InterPro; IPR012008; PPEF.
InterPro; IPR016186; T_phtase anau Pfam; PF00036: afta-
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Pfam; PF000612; IQ; 1.
Pfam; PF00149; Metallophos; 1.
PIRSF; PRISF000912; PPBF; 1.
PRINTS; PR00114; STPHPHTASE.
ProDom; PD000012; EF-hand; 1.
ProDom; PD0000252; T phtase_apaH; 1.
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SMART; SM00015; IQ; 1.

SMART; SM00156; PP2AC; 1.

SMART; SM00156; PP2AC; 1.

PROSITE; PS00018; EP HAND; UNKNOWN_2.

PROSITE; PS50096; IQ; 1.

PROSITE; PS50096; IQ; 1.

PROSITE; PS00125; SER THR. PHOSPHATASE; UNKNOWN PROSITE; PS00125; SER THR. PHOSPHATASE; UNKNOWN PROSITE; PS00125; SER THR. PHOSPHATASE; UNKNOWN PROSITE; PS00125; SER THR. PHOSPHATASE; UNKNOWN PROSITE; PS00125; SER THR. PHOSPHATASE; UNKNOWN PROSITE; PS00125; SER THR. PHOSPHATASE; UNKNOWN PROSITE; PS00125; SER THR. PHOSPHATASE; UNKNOWN PROSITE; PS00125; SER THR. PHOSPHATASE; UNKNOWN PROSITE; PS00125; SER THR. PHOSPHATASE; UNKNOWN PROSITE; PS00125; SER THR. PHOSPHATASE; UNKNOWN PROSITE; PS00125; SER THR. PHOSPHATASE; UNKNOWN PROSITE; PS00125; SER THR. PHOSPHATASE; UNKNOWN PROSITE; PS00125; SER THR. PHOSPHATASE; UNKNOWN PROSITE; PS00125; SER THR. PHOSPHATASE; UNKNOWN PROSITE; PS00125; SER THR. PHOSPHATASE; UNKNOWN PROSITE; PS00125; SER THR. PHOSPHATASE; UNKNOWN PROSITE; PS00125; SER THR. PHOSPHATASE; UNKNOWN PROSITE; PS00125; SER THR. PHOSPHATASE; UNKNOWN PROSITE; PS00125; SER THR. PHOSPHATASE; UNKNOWN PS00125; SER THR. PHOSPHATASE; UNKNOWN PS00125; SER THR. PHOSPHATASE; UNKNOWN PS00125; SER THR. PHOSPHATASE; UNKNOWN PS00125; SER THR. PHOSPHATASE; UNKNOWN PS00125; SER THR. PHOSPHATASE; UNKNOWN PS00125; SER THR. PHOSPHATASE; UNKNOWN PS00125; SER THR. PHOSPHATASE; UNKNOWN PS00125; SER THR. PHOSPHATASE; UNKNOWN PS00125; SER THR. PHOSPHATASE; UNKNOWN PS00125; SER THR. PHOSPHATASE; UNKNOWN PS00125; SER THR. PHOSPHATASE; UNKNOWN PS00125; SER THR. PHOSPHATASE; UNKNOWN PS00125; SER THR. PHOSPHATASE; UNKNOWN PS00125; SER THR. PHOSPHATASE; UNKNOWN PS00125; SER THR. PHOSPHATASE; UNKNOWN PS00125; SER THR. PHOSPHATASE; UNKNOWN PS00125; SER THR. PHOSPHATASE; UNKNOWN PS00125; SER THR. PHOSPHATASE; UNKNOWN PS00125; SER THR. PHOSPHATASE; UNKNOWN PS00125; SER THR. PHOSPHATASE; UNKNOWN PS00125; SER THR. PHOSPHATASE; UNKNOWN PS00125; SER THR. PHOSPHATASE; UNKNOWN PS00125; SER THR. PHOSPHATASE; UNKNOWN PS00125; SER THR. PHOSPHAT
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Q9W6R4;
01-NOV-1999 (
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EMBL; AP146697; AAD28796:1; -; Genomic_DNA.
HSSP; P02588; 1TNX.
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Prugu rubripes (Japanese pufferfish) (Takifugu rubripes).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Takifugu.
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01-NOV-1999 (TrEMBLrel. 12,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ensembl; SINFRUGO0000152266; Fugu rubripes
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
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       116 RGNRLHPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVC-GDLHGKLDDLLVVLHKNG
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                                                                                   74
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                                                                           LNGNGPDLISKLMDSASDPWLENENCYNLVTVPETYTGPRLSFPLSVSDMNALLGAFKEQ
                                                                                                                                                   AAGRK----NQYQGSAHVSVLDDKD--DLVEBFGDIVNAKIBLPIRKNHIDLLIDVFRKK
                                                                                                                                                                                                                               EKTAÍKAAVLÍ ÓRWVRRYMARLEMRRRYTWNÍ FÓSI EY AGEÓDÓLOLSS FFS FMLNINVTH
                                                                                                                                                                                                                                                                           HIDDSQVNKLANIMDLNKDGSIDFNEFLKAFYV--VHRYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AYSKAEMLEKCRMMDLNGDGKVDLNEFLEAFRLSDLHRKE
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            NUCLEOTIDE SEQUENCE.

NUCLEOTIDE SEQUENCE.

A Malceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

Nicaud S., Jaffe D., Fischer S., Lutfalla G., Dossat C., Segurens B.,

Nicaud S., Jaffe D., Fischer S., Lutfalla G., Dossat C., Segurens B.,

Nicaud S., Jaffe D., Fischer S., Lutfalla G., Dossat C., Segurens B.,

Nicaud S., Jaffe D., Fischer S., Loudet N., Castellano S.,

Nicaud S., Jaffe D., Fischer S., Boudet N., Castellano S.,

A Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

Na Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

Na Cruaud C., Shalli Z., Cattolico L., Poulain J., De Berardinis V.,

Na Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

Na Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

Na Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

Na Cruaud C., Duprat S., Brottier P., Cottanceau J.P., Gouzy J.,

Na Parra G., Lardier G., Chapple C., McKernan K.J., McSwan P., Bosak S.,

Na Parra G., Lardier G., Chapple C., McKernan K.J., McSwan P., Bosak S.,

Na Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

Na Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,

Na Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,

Na Mincker P., Lander B.S., Weissenbach J., Roest Crollius H.;

The early vertebrate proto-karyotype.";

Na Laudet V., Schachter V., Gertier F., Saurin W., Scarpelli C.,

Na Mincker P., Lander B.S., Weissenbach J., Roest Crollius H.;

The early vertebrate proto-karyotype.";

Na Laudet V., Schachter V., Gertier F., Saurin W., Scarpelli C.,

Na Marcher P., Lander B.S., Weissenbach J., Roest Crollius H.;

Na Marcher P., Lander B.S., Weissenbach J., Roest Crollius H.;

Na Marcher P., Lander B.S., Weissenbach J., Roest Crollius H.;

Na Marcher P., Lander B.S., Weissenbach J., Roest Crollius H.;

Na Marcher P., Lander B.S., Weissenbach M., Roest Crollius H.;

Na Marcher P., Lander B., Weissenbach M., Roest Crollius H.;

Na Marcher P., Lander B., Weissenbach M., Ro
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7 TETNG
QASHR7_TETNG PRELIMINARY; PRT; 671 AA.
QASHR7;
13-SEP-2005 (TERMELrel. 31, Created)
13-SEP-2005 (TERMELrel. 31, Last sequence update)
13-SEP-2005 (TERMELrel. 31, Last annotation update)
13-SEP-2005 (TERMELrel. 31, Last annotation update)
Chromosome 5 SCAF14581, whole genome shotgun sequences
                                                                                                                                                                                                                                                                                                                                                                ORFNames=GSTENGO0018033001;
Tetraodon nigroviridis (Green puffer).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Eukaryota, Metazoa; Chordata; Teleostei; Buteleostei; Neoteleostei;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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QARUII_TETNG PRELIMINARY; PRT; 797 AA.

QARUII;

13-SEP-2005 (TrEMBLrel. 31, Created)

13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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Genoscope; Whitehead Institute Centre for Genome Rese

Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databas

-I- CAUTION: The sequence shown here is derived from

EMBL/GenBank/DDBJ whole genome shotgun (WGS) entr

preliminary data.

EMBL. Caarol 01451: Caroosis 1.... Genomic DNA
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NIDFNEFLEAFRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ETPYVFNGDFYDRGKNSIEVVVLLFAYLLLYPDYMHLNRGNHEDHLMNLRYGFTKSVMQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNPYVFNGDFVDRGKRGLEVLLLLSLYLAFPNAVFLNRGNHEDSVMNARYGFIREVESK
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                                   KVDLNEFLEAFRL
                                                                                                                                                                                      HWCKVMENVTKLGLPWRLLRDKLAPGTDSQKVNYNRTLDLLDTDVILEAEADGMSVMDAL
                                                                                                                                                                                                                                                                                                                       DNFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRLNNQLMPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGPDLISKIMDSASDSWMENENCYNFVSVPETYTGPRLSFPLSLPDMNALLSAFKERQ--
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                                                                           FRYRKDIBIIFNIIDKDHSGLISIBBFRHTWHLFSAHLGVKIDNRAIDDLARSIDFNKDG
                                                                                                             YANKASLVAIFNIIDADNSGEITLDEFETAIDLLVAHMPGAYSKAEMLEKCRMMDLNGDG
                                                                                                                                                  EWAQVLETGLRLELPWRTLRPHLARLASDGRVEYHSCFEDMEPGIPLVQVTPNLA--EAL
                                                                                                                                                                                                                           FYQY-QVSRFTRKLTLTQRVRAAEGSALRALKEKLFTHRSELILGFQQYDHNNTGTILVS
                                                                                                                                                                                                                                                             FVQYISAASQTKRLSFKQRMGIVESSALKELAVRMRDHRDELEDBFRKYDPKDSGYISIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGFSDSTSLDLIKSIDRGK-----
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671 AA,
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databases.
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genome shotgun sequence

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RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Siemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Cruaud C., Duprat S., Chapple C., McKernan K.J., McSwan P., Bosak S.,
RA Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA Laudet V., Schachter V., Quetier P., Saurin W., Scarpelli C.,
RA Wincker P., Lander B.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
The early vertebrate proto-karyotype.";
U. Nature 431:946-957(2004).
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NON_TER
SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
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L; CAAE01014996; CAG08121.1; -; Genomic_DNA
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                                                                                                                                                                                                                                                                                     NNKKNPRVENNCALQNGMPSLEKPYVENGDEVDRGRDSIBILVILFAFLLVYPSDVYLNR
GTRTSFQNRSLQDFSDRIRLPABNELELRRRREFIFHLSESEKTINPAASSDSVKSESLK
                                                  D-----
                                                                                                                                             TSLDLIKSIDRGKYVSILRPP------
                                                                                                                                                                                          GNHEDHIVNLRYGFTKEVLTKYKMHGKRILKLLQKIFSWLPLATVIDQKVLVLHGGISDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKRGNRLHPKYVALILRBAAKSLKQLPNISPVSTAVSQQVTVC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ERNLI----SHIFRENEVCRDAEWERYFCYKNIEVPEIYSGPHLTFPLTVEQAVGLVEAFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKNQYQGSAHVSVLDD--KDDLVEEFGDIVNAKI------ELPIRKNHIDLLIDVFR
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                                                                                             TDLGLLAKLDRHNYVSALR PPKRRGYNSAGTSIDSDVDEDVSCNSKI FQRRTSLTYAR PL
                                                                                                                                                                                                                                                                                                                                                                                   GFTLPKTVLRTWVAAPIGDLHGQLEDLLLIFYKVRNPLPLFYMFSPTVVFLHVTYEQTSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NKK--QLHSRYILQLLLETWKLLRMLPNINRISTCHSKEITICGELQEGFGNGGLCREIV
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797 AA;
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91973 MW;
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32.5%;
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Best Local S
Matches 227
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WormPep; F23H11.8b; CB30662.
GO; GO:0005509; F:calcium ion binding; IF GO; GO:0016787; F:hydrolase activity; IEB InterPro; IPR011992; EF-Hand type.
InterPro; IPR002048; EF_hand_Ca_bd.
InterPro; IPR006186; T_phtase_apaH.
                                                                                                                                                                                                         PRINTS; PRO0114; STPHPHTASE.
SMART; SM00054; BPL; 3.
SMART; SM00156; PPLAC; 1.
PROSITE; PS00018; EF HAND; UNKNOWN 2.
PROSITE; PS00125; SER_THR_PHOSPHATASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Phosphatase with ef hands protein 1, isoform b.
Name=pef-1; ORFWames=F23H11.8;
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QBMYR2;
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Pfam; PF00149; Metallophos; 1.
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MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ensembl; F23H11.8; Caenorhabditis elegans.
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Science 282:2012-2018(1998)
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                           81 KDDLVEEFGDIVNAKIE-
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                                                                           Conservative
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                                                                                                                                                                      65150 MW;
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                                                                                               33.3%;
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Pred. No. 3.3e
06; Mismatches
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Query Match
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Matches 159
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 3 similar to human protein phosphatase,
14-SEP hand calcium-binding domain 1 (PPEF1), transcript variant 1,
14-SEP-2004 (Cynomolgus monkey)
15-SEP-2005 (Tremates) (Cynomolgus monkey)
16-SEP-2005 (Tremates) (Cynomolgus monkey)
17-SEP-2005 (Tremates) (Cynomolgus monkey)
18-SEP-2005 (Tremates) (Cynomolgus monkey)
18-SEP-2005 (Tremates) (Cynomolgus monkey)
19-SEP-2005 (Tremates) (Cynomolg
                                                                                                             Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y., Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.; "Substitution rate and structural divergence of 5'UTR evolution: Comparative analysis between human and cynomolgus monkey cDNAs." Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; AB179074; BAE02125.1; -; mRNA.

SEQUENCE 405 AA; 46636 MW; ClE9889F20B23B4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                               International consortium for macaque cDNA "DNA sequences of macaque genes expressed evolutionary implications ", submitted (JUN-2005) to the EMBL/GenBank/E
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                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLVRSHECKFEGYEFSHNNTCLTVFSASNYYETGSNRGAYVKFIGKSKQPHFVQYM--AS
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                                                                                                                                                                                                                                                                                                                         SEQUENCE.
      Conservative
                              41.3%;
                                                         24.4%;
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                              Score 839; DB 2;
Pred. No. 1e-42;
      Mismatches
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                                                         Length 405;
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RX KITARLE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Magner L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Magner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Magner L., Shenmen C.M., Schuler G.D.,
RA Lackhul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Raha S.S., Loquellano N.A., Peters G.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Butterfield Y.S.N., Krzywinski M.I., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RGeneration and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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Bukaryota; Metazoa; Chordata; Craniata; Vereabrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
NCBI_TaxID=8364;
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Q68EP0;
25-OCT-2004 (TrEMBLrel, 2
Klein S., Gerhard D.S.;
Submitted (AUG-2004) to
-!- CATALYTIC ACTIVITY:
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   the EMBL/GenBank/DDBJ databases A phosphoprotein + H(2)O = a pr
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R SNR; Q68EP0; 20-493.

R SNR; Q68EP0; 20-493.

R Ensembl; ENSXETG0000018265; Xenopus tropicalis.

R G0; G0:0005737; C:cytoplasm; IEA.

R G0; G0:0005634; C:nucleus; IEA.

R G0; G0:00016787; P:hydrolase activity; IEA.

R G0; G0:0004721; P:hydrolase activity; IEA.

R G0; G0:0004721; P:protein amino acid dephosphorylation; IEJ.

InterPro; IPR011236; PPPEase.

InterPro; IPR011236; PPPEase.

InterPro; IPR011290; TPR-like_helical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 135; Conserv
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Pfam; PF00515; TER 1; 3.

PIRSF; PIRSF033096; PPPCase 5; 1.

PRINTS; PR00114; STPHPHTASE.

ProDom; PD000252; T_phtase_apaH; 1.

SMART; SM00156; PP2AC; 1.

SMART; SM00156; TPR; 3.

PROSITE; PS00125; TER; 3.

PROSITE; PS00125; TER; 3.

PROSITE; PS50293; TPR; 3.

PROSITE; PS50293; TPR; 3.

PROSITE; PS50293; TPR; 3.

PROSITE; PS50293; TPR; 3.
                                                                                  13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Serine/threenine protein phosphatase-like protein (ORFNames=LmjFl2.0660;
 NUCLEOTIDE SEQUENCE.
STRAIN=Friedlin;
Peacock C.S., Murphy
                                                                                                                                         Q4QGM7; LEIMA PRELIMINARY; Q4QGM7;
                                             Leishmania major.
Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
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SEQUENCE
                                                                                                                                                                    LEIMA
18
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SIMILARITY:
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|:||:||:||:||:|||||
QIRSIERNR-----QPP--DSGPM------CDLLWSDPQPQDG-RSSSKRGVSCQFGP
                                                                                                                                                                                                                                                                                 DVTDNFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRLN-NQ
                                                                                                                                                                                                                                                                                                                                                          TMNQMYGFEGEVKAKY---SAQMFQLFSEVFQWLFLAMCVNQRVLIMHGGLFSEDGVTLD
                                                                                                                                                                                                                                                                                                                                                                          VMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGF--SDSTSLD
                                                                                                                                                                                                                                                                                                                                                                                                        YDLMNIPHLNGLPSENNPYIPNGDFVDRGSFSVEVIVTLFGFKLLYPAQFHLLRGNHETD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDLLIDVFR-KKRGNRLHPKYVALILRBAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKL
                                                                                                                                                                                                                                          LMPHFVQY 408
                                                                                                                                                                                                                                                               DVTRRFLEENGLDYIIRSHEVKPEGYEVSHNGLCVTVFSAPNYCDQMGNKGAYIHLNGSD
                                                                                                                                                                                                                                                                                                                                                                                                                                DDLLLVVLHKNGLPSSSNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDFMLELMQFYKDQKKLHRKCVYQMLVQVKDILSKLPSLVEISLEKSQQVTVCGDTHGQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Iron; Re
493 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.2%;
ilarity 43.8%;
Conservative 48
  Muzphy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Belongs to the PPP phosphatase AAH80162.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeāt; TPR repeat.
A; 56247 MW; DD7597B849DD40EF CRC64;
  ۲.,
                                                             Kinetoplastida;
   Ivens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 627.5; 1
Pred. No. 9.4e
48; Mismatches
  A.C.,
                                                                                                                                                         PRT;
   Berriman
                                                                                                                                                         897
                                                            Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ).4e-30;
nes 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length
3
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  Blackwell
                                                                                               (BC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              493;
                                                             Leishmania
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042205_XEN
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NUCLEOTIDE SEQUENCE.
Ollendorff V., Donoghue
                                             Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Ve;
Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus; Xenopus.
                                                                                                      01-JAN-1998 (TrEMBLrel. 05, Crea
01-JAN-1998 (TrEMBLrel. 05, Last
01-WAR-2004 (TrEMBLrel. 26, Last
Protein phosphatase 5 (Fragment)
                                                                                                                                                     042205 XENLA PRELIMINARY;
                                                                                               Name=PP5
                                  NCBI_TaxID=8355
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Query Match
Best Local S
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EMBL; CT005251; CAJ02710.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase.
SEQUENCE
                XBNLA
                                                                                                         624
                                                                                                                                        731
                                                                                                                                                                     564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       316 IMWSDPQATMGCVPNTLRGAGVWFGPDVTDNFLQRHRLSYVIRSHECKPNGHEFMHDNKI ::|| ::| ::|| ::|| ::|:| ::|:|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           274 GARVENGRVIQGCKVVVVGDLHGQIADLLHILKESGMPSESNYYVFNGDYVDRGACGVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 SQQVT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 ITIFSASNYYAIGSNKGA---YIRLNNQLMPHFVQY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGSVLNSRVLIVHGG--FSDSTSLDLIKSIDRGKYVSILRPPLTDGEPLDKTEWQQIF-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIDAMEQL
                                                                                                       ATDPVTLL
                                                                                                                                                                                                                 BABADGMSVMDALYA----NKASLVAIENIIDADNSGEITLDEF---ETAIDLLVAHMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MLWSDPVEDIKSWRESQRGAGVEFGSDVTMEFLENNKLELIVRSHEDCLSGYEEHHNHKL
                                                                                                                                      ---SDCQLFQLFESFDEKGNGHISGPEFL-----
                                                                                                                                                                   GAYSKAEMLEKCRMMDLNGDGKVDLNEFLEAFRLSDLHRKEQQDENIRRRSTGRPSVAKT
                                                                                                                                                                                                  WGBEWRQSVCARVLQQQRMNHRSQLVSA----AFNKEVVNYNEFCSVMRAIDYTT----
                                                                                                                                                                                                                                                                TNKGSLWMIEWVBSMRNVLNLDLPWYFLRGYLVBVDDHSRIWYAPFLNRFHNVLQD----L
                                                                                                                                                                                                                                                                                             KDSGYISISHWCKVMENVTKLGLPWRLLRDKLAPGTDSQKVNY----NRTLDLLDTDVIL
                                                                                                                                                                                                                                                                                                                           ARISSFTATVGSVGFGVSKSNFMSRVLLHRRTKDNILRELRERIYORRHRLLAYFSKLDR
                                                                                                                                                                                                                                                                                                                                                            TKRLSFKQRMGIV-----
                                                                                                                                                                                                                                                                                                                                                                                         LTVFSASNYDGPNSNYGAICTFIGDNPEPSYHTYOMFEDEYDDSQVVSLTDSFTLTAPNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LATLIGGKIFVVHGGPPRRRGVSINDISRIQRFRQIPI-----PNYSQPEEDEIFQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                         631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103525 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -VCGDLHGKLDDLLVVLHKNGLPSSSNPYVFNGDFVDRGKRGLEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 618.5; I
Pred. No. 7.2e-
88; Mismatches
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16381EB67C70D4F1
                                                                                                                                                                                                                                                                                                                                                            ----ESSALKELAVRMRDHRDELEDEFRKYDP
492
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A
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                                                                                                                                      -KKVQQIAN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Barrell
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                                                                                                                                      -GKPDPLRW
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                                                                                                                                                                                                  730
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Last sequence up

update)

update)

Vertebrata; Euteleostomi;

Pipoidea;

Created)

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RESULT 20
Q6GP86 XEN
ID Q6GP8
AC Q6GP8
DT 05-JT
DT 05-JT
DT 05-JT
DT 05-JT
DE PP5 I
CN Name:
OR Xenoj
OC Euka;
OC Amph:
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Best Local Sim:
Matches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR011236; PPPtase_5.
InterPro; IPR006186; T_phtase_apaH.
InterPro; IPR006186; TPR.
InterPro; IPR011990; TPR-like_helical.
Pfam; PF00139; Metallophos; 1.
Pfam; PF00515; TPR_1 3.
PIRSP; PIRSF033096; PPPtase_5; 1.
PIRSP; PRR00114; STPPHFRASE.
PRODOm; PF0000252; T_phtase_apaH; 1.
SMART; SM00156; PPPAC; 1.
SMART; SM00156; PPPAC; 1.
                                                                             05-JUL-2004
05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6666668
866668
Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00125; SER THR PHOSPHATASE; UNKNOWN 1.
PROSITE; PS50005; TPR; 3.
PROSITE; PS50293; TPR REGION; 1.
Hydrolase; Iron; TPR repeat.
NON_TER 1 1
                                                                                                                         QGGPS6 XENLA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases. 
 -i- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein
                                                   Name=PP5;
                                                              PP5 protein.

    -I- SIMILARITY: Belongs to the PPP phosphatase family.
    EMBL; AF018263; AAB70574.1; -; mRNA.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR004843; M-pesterase.
                                                                                                                                                              XENLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO:0005737; C:cytoplasm; IEA.
GO:0005634; C:nucleus; IEA.
GO:0005488; F:binding; IEA.
GO:0016787; F:hydrolase activity; IEA.
GO:0016781; F:phosphoprotein phosphatase activity; I
GO:0004721; F:phosphoprotein amino acid dephosphorylation;
GO:0006470; P:protein amino acid dephosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphate.
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         042205; 19-492.
                                                                                                                                                                                                                                                       401
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                                                                                                                                                                                                                                                                                                                                                                                 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                            LIKSIDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMGCVPNTLRGAGVWFGP
                                                                                                                                                                                                                                                                                                                                                                                                                                          VMNARYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGF--SDSTSLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDLLVVLHKNGLPSSSNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDS
                                                                                                                                                                                                                                             LMPHFVQY 408
                                                                                                                                                                                                                                                                                  DVTHQFLEENGLDYIINSHEVKPEGYEVSHNGLCVTVFSAPNYCDQMGNKGAYIHLSGSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YDLMNI FHLNGLPSENNPY I FNGDFVDRGSFSVEVI VTLFGFKLLY PAHFHLLRGNHETD
                                                                                                                                                                                                                                                                                                                 DVTDNFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRLN-NQ 400
                                                                                                                                                                                                                                                                                                                                                 QIRNIERNR-----QPP--DSGPM-----CDLLWSDPQPQDG-RSTSKRGVSCQPGP
                                                                                                                                                                                                                                                                                                                                                                                                             TWNQMYGFEGEVKAKY---SAQMFQLFSEVFQWLPLAMCVNQRVLIMHGGLFSEDGVTLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             492 AA; 56145 MW; 86EF80641C33DD16 CRC64;
                                                                               (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last seq
(TrEMBLrel. 27, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50;
                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 615.5;
Pred. No. 5e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 103;
                                                                                                                                            493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K.J., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA RA Rating M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rating M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.,
Tomeration and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                 phosphate.

C -|- SIMILARITY: Belongs to the PPP phosphatase family.

EMBL, BC073033, AAH73033.1; -; mRNA.

R BC073033, AAH73033.1; -; mRNA.

R GO; GO:0005737; C:cytoplasm; IEA.

R GO; GO:0005737; C:cytoplasm; IEA.

R GO; GO:0005737; F:hydrolase activity; IEA.

R GO; GO:0005721; F:phydrolase activity; IEA.

R GO; GO:0004721; F:phosphoprotein phosphatase activity; IEA.

R GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.

R GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.

R InterPro; IPR004843; M-pesterase.

R InterPro; IPR004843; M-pesterase.

R InterPro; IPR004843; M-pesterase.

R InterPro; IPR004843; TPR.

R InterPro; IPR001440; TPR.

R InterPro; IPR01140; TPR.

R InterPro; IPR01140; TPR.

R InterPro; IPR01140; TPR.
Query Match
Best Local Similarity
Matches 132; Conserv
                                                                                         Pfam; PF00149; Metallophos; 1.

Pfam; PF00149; Metallophos; 1.

PFAM; PF00515; TPR 1; 3.

PFNSF; PIRSF033096; PPDtase_5; 1.

PFNSF; PR00114; STPHPHTASE.

PFCDom; PD000252; T phtase_apaH; 1.

R SMART; SM00126; PP2Ac; 1.

R SMART; SM00126; TPR; 3.

R PROSITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.

R PROSITE; PS0005; TPR; 3.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klein S., Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
-i- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8355;
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174; Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lichardson P.;
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Conservative
17.9%; Score 615.5; DB
42.9%; Pred. No. 5e-29;
Live 50; Mismatches 1
                                                  DB 2;
  103;
     Indels
                                                  Length
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                                                       493;
  23;
Gaps
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105 IDLLIDVFR-KKRGNRLHPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKL

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            -1- SIMILARITY: Belongs to the PPP phosphatase family.

EMBL; AAAB01008880; EAA08659 2; -; Genomic_DNA.

RGO; GO:0005737; C:cytoplasm; IEA.

RGO; GO:0005737; C:cytoplasm; IEA.

RGO; GO:0005637; F:nycophoprotein phosphatase activity; IEA.

RGO; GO:00064721; F:phosphoprotein phosphatase activity; IEA.

RGO; GO:0006470; P:protein amino acid dephosphorylation; IEA.

RGO; GO:0006470; P:protein amino acid depho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q7QB71 ANOGA
Q7QB71;
01-MAR-2004 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2004 (TrEMBLrel. 26, Creat
01-MAR-2004 (TrEMBLrel. 26, Last
01-MAR-2004 (TrEMBLrel. 26, Last
01-MAR-2000 (TrEMBLrel. 26, Last
ENSANGPO0000011234 (Fragment).
ORFNames=ENSANGG00000008745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Anopheles gambiae Sequence Committee; Submitted (APR-2004) to the EMBL/GenBank/DDBJ-1- CAPALYTIC ACTIVITY: A phosphoprotein + H(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anopheles gambiae str. PEST.
Eukaryota, Metazoa; Arthropoda, Hexapoda; Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Culicidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-PEST
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                                                                                                                                                                                                                                                                                                                                                                                                                       preliminary SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                phosphate.
CAUTION: The sequence shown here is derived EMBL/GenBank/DDBJ whole genome shotgun (WGS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anopheles gambiae Sequence Committee;
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                                                           NUCLEOTIDE SEQUENCE.

NUCLEOTIDE SEQUENCE.

A Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,

A Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

A Mauceli E., Bouneau L., Fischer S., Lutfalla G., Dossat C., Segurens B.,

A Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

A Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,

A Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

A Anthouard C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

A Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

A Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,

A Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,

A Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gonzy J.,

A Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Bosak S.,

A Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,

A Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,

A Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,

A Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,

A Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

A Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

A Lindblad-Toh K., Birren B., Nusbaum C., Saurin W., Scarpelli C.,

A Mincker P., Lander B.S., Weissenbach J., Roest Crollius H.;

Thomas duplication in the teleost fish Tetraodon nigroviridis reveal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local 9
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                    Tetraodon nigroviridis (Green puffer).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 16 SCAF15113, whole genome shotgun seque
  the early vertebrate
Nature 431:946-957(20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Fragment).
ORFNames=GSTENG00035185001;
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                     rly vertebrate proto-karyotype.
431:946-957(2004).
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Similarity 36.4%;
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Pred. No. 5.5
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RESULT 23
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Best Local S
Matches 161
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R Pfam; PF00149; Metallophos; 1.

R Pfam; PF05485; THAP; 1.

R Pfam; PF00545; TPR 1; 3.

R Pfam; PF00515; TPR 1; 3.

R PRODOm; PD00114; STPHPHTASE.

PRODOm; PD000252; T_phtase_apaH; 1.

SMART; SM00692; DD3; 1.

SMART; SM00692; DD3; 1.

SMART; SM00028; TPR; 3.

PROSITE; PS00125; SER THR PHOSPHATASE; UN
PROSITE; PS50015; TPR; 3.

PROSITE; PS5005; TPR; 1.

PROSITE; PS5005; TPR REGION; 1.

Hydrolase; Iron; TPR repeat.

NON TER
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-I- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry whi
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SIMILARITY: Belongs to the PPP
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                                                               478
                                                                                            461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                    RHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRL-NNQLMPHFVQY
                                                                                                                                                                                                                                           R-----QPP--DSGPM-----CDLLWSDPQPQNG-RSISKRGVSCQFGPDVTERFLS
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                                                               CSVPN-CK--
                                                                                           ISISHWCKVMENVTKLGLPWRLLRDKLAPGTDSQ 494
                                                                                                                                                                                                                                                                       KYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMGCVPNTLRGAGVWFGPDVTDNFLQ
                                                                                                                                                                                                                                                                                                 EGEVKAKYT----AQMFQLFSEVFQWLPLAQCINNKVLVMHGGLFSEDGVTLEDLRKIDRN
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                                                                                                                       -DLTTVHBFAFTLFLIQLVTGGDHRRQM----
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5; Mismatches
                                                             NGSGPGTDKK
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Best Local Similarity
Matches 196; Conserv
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Science 307:82-86(2005).
-i- CAUTION: The sequence shown here is derived in EMBL/GenBank/DDBJ whole genome shotgun (WGS) preliminary data.

EMBL; CAAJ01001923; CAH77292.1; -; Genomic DNA.
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Q4YOL8;
[31-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
PP1-11ke protein serine/threonine phosphatase, putative.
ORPNames=PC000121.0:0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium chabaudi.
Eukaryota; Alveolata;
NCBI_TaxID=5825;
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NCE 953 AA; 111137 MW; 2C224CE0D1667B
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                       DADNSGEITLDEFETAIDLLVAHMPGAYSKAEMLEKCRMMDLNG------DGKVDLN
                                                                                                                                                                                                                                                                                                                                                                     RLINIQLMPHFVQYISAASQTKRLSF----KQRMGIVESSALKE------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WFGPDVTDNFLQRHRLSYVIRSHECKP--NGHBFMHDNKIITIFSASNYYAIGSNKGAYI
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                                                                                                                                                                                                   LNDILNFLSTLICNEKNNLWNNLYBKDKGNTGEVHINIWREBLEKLTKAKNVPWIYLCKK
                                                                                                                                                                                                                                                                                                                I FNQDLTFEVHEYMSPSLDVIRETFEENQKLREKVLNSSNLLEVEKNEQRNAKSIPPDAA
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                                                                                     FKM-IENNHVNYNNILSRFKINYDPSKKCLKSEWKNECFEHLYEALLKADLSLRETLMIF
                                                                                                                                          LAPGTDSQKVNYNRTLDLLDTDV-----ILBABADG---MSVMDALYANKASLVAIFNII
                                                                                                                                                                                                                                                  -----LAVRMRDHRDBLBDBFRKYDPKDSGYISISHWCKVMENVTKL-GLPWRLLRDK
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Pred. No. 6.3e-28;
2; Mismatches 264;
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Best Local Sim
Matches 174;
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GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR011992; EF-Hand type.
InterPro; IPR002048; EF_hand Ca_bd.
InterPro; IPR004843; M-pesterase.
InterPro; IPR006186; T_phtase_apaH.
Pfam; PF00149; Metallophos; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0114; STPHPHTASE.

ProDom; PD000252; Thtase_apaH; 1.

SMART; SM00156; PP2A; Thr. PHOSPHATASE; UNKNOWN 1.

PROSITE; PS00125; SER THR PHOSPHATASE; UNKNOWN 1.

SEQUENCE 923 AA; 104798 MW; 95E6646BE32B2143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Andersson B., Bontempi B.J.;
Submitted (JUN-2003) to the EMB
EMBL, AC137988; AAN78342.1; -;
HSSP; P36873; 11T6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98391765; PubMed=9724326; Andersson B., Aslund L., Tammi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003
01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete sequence of a 93.4-kb contig from chromosome Trypanosoma cruzi containing a strand-switch region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pettersson U.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trypanosoma cruzi.
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TRYCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                    TKYDRN---VFRLVQRCFCALPLATIIGKKVFVVHGGLPRRKGVNIEDISRIQRFRQI--
                                                                                                                                                                               SKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGF--SDSTSLDLIKSIDRGKYVSI
                                                                                                                                                                                                                                                      SSSNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNARYGFIREVE
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SYVIRSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAY-IRLNNQLMPHFVQYISAA
                                             ---PMPD---YSQPEEDEIFQDLLWSDPVEDLQGWRESPRGAGVVFGADVTQEFLQNNGL
                                                                                                                                                                                                                            NEGTYY I FNGDF V DRGANGVEVIL I LFSLMLACPKYVTLNRGNHECDYMNDEYGFDVEVS
                                                                                                                                                                                                                                                                                                                    VFTDAMSHLNTMPNVVRLSPPVGARVSNGRINQGSKVVVVGDLHGQLADLLHILKECGMP
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                                                                                       LRPPLTDGEPLDKTEWQQIF-DIMWSDPQATMGCVPNTLRGAGVWFGPDVTDNFLQRHRL
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Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 594.5; DB 2;
Pred. No. 2.1e-27;
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RESULT 2 Q512P5 ID DE P1 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7 13 D7
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X PubMed=15729342; DOI=10.1038/nature03291;

X Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,

Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,

Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.

A Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,

Na Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,

Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,

Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,

A Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,

A Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,

A Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,

A Quallen N., Glothrist C., Stroup S.E., Bhattacharya S., Lohia A.,

Challen N., Glichrist C., Stroup S.E., Bhattacharya S., Lohia A.,

A Poster P.G., Sicheritz-Ponten T., Weber C., Singh U., Mukherjee C.,

B L-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,

"The genome of the protist parasite Entamoeba histolytica.";

Nature 433:865-86(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 143; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary data.
EMBL; AAFB01000329; E
SEQUENCE 473 AA: 5
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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Q512P5 ENTHI PRELIMINARY;
Q512P5;
Q512P5;
Q512P5;
Q512P5;
Q512P5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein phosphatase, putative. ORFNames=90.t00028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota;
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                                                                                                                                                                                                                                          116 RREQLFFEA-ISVEDEKQTISWRDIDASTSTIKIEDDKPITKENVQ---EIYEAMKSNCQ
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                                       LPSSSNPYVFNGDFVDRGKRGLEVLLLLLSLYLAFPNAVFLNRGNHEDSVMNARYGFIRE
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                                                                                                                                                                   ----rlhpkyvalilreaaksikqlpnispvstavsqqvtvcgdlhgkdddilvvlhkng
                                                                                                                                                                                                                                                                                                          RKNOYQGSAHVSVLDDKDDL----VEEFGDIVNAKIELPIRKNHIDLLIDVFRKKRGN--
                                                                                                                                                                                                                                                                                                                                                                              FVKGYYRQASAFAALGQLQEAISAC-----BKAKKLSPKD-----GMINSMLKGLKEK--
                                                                                                                                                                                                                                                                                                                                                                                                                                             FIOKWYRRHOA-----RREMORRCNWOIFONLEYASBODOABLYKFFNDLIKHMPOAAG
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53606 MW; (
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Score 582.5; DB:
Pred. No. 4.8e-27
4; Mismatches 13
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665B460BC0ED93A8
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R Bisembl; Y39B6A.2; Caenorhabditis elegans.

R WormBase; WBGeneO0012665; Y39B6A.2.

R WormBase; WBGeneO00126619.

R GO; GO:0005737; C:cytoplasm; IEA.

R GO; GO:0005534; C:nucleus; IEA.

R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0004721; F:phodploase activity; IEA.

R GO; GO:0004721; F:phosphoprotein phosphatase activity; IEA.

R GO; GO:0004721; F:phosphoprotein phosphorylation; IEA.

R GO; GO:0004721; F:phosphoprotein phosphotase activity; IEA.

R InterPro; IPR00143; M-pesterase.

R InterPro; IPR001440; TPR.

R InterPro; IPR001440; TPR.

R InterPro; IPR001440; TPR.

R InterPro; IPR00149; Metallophos; 1.

R Pfam; PF00149; Metallophos; 1.

R Pfam; PF00149; Metallophos; 1.

R PRINTS; PR00114; TPR 1; 2.

R PRINTS; PR001515; TPR 1; 2.

R PRINTS; PR00152; TphPHTASE.
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Matches
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein Y39B6A.2.
ORFNames=Y39B6A.2.
                                                                                                                                                                                                                                                                   PROSITE; PS50005; TPR; 2.
PROSITE; PS50293; TPR REGION; 1
Complete proteome; Hypothetical
SEQUENCE 496 AA; 56462 MM; 2
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                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P53041; 1A17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The C. elegans sequencing consortium; "Genome sequence of the nematode C. e
                                                                                                                                                                                 Local
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                                                                                                                                                     137;
                                 98
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SM00028; TPR; 2.
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                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                proteome; Hypothetical protein.
496 AA; 56462 MW; 2C872FF1700384EE CRC64;
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                                 DNAI---AIDPSYVKGFYRRATANMALGRFKKALTDYQAVVKVCPNDKDARAKFDECSKIV
                                                                               ENAIRAAI---FIQKWYRRHQARREMOR-RCNWQIFQNLEYASEQDQAELYKF--FNDLI
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                                                                                                                                                     Conservative
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                                                                                                                                                                           16.9%;
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                                                                                                                                            Score 581; DB 2;
Pred. No. 6.3e-27;
'7; Mismatches 167
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Q4Z5E3;
13-SEP-2005 (TrEMBLrel. 3:
13-SEP-2005 (TrEMBLrel. 3:
                                                                                                                                                                  PRINTS; PR00114; STPHPHTASE.

ProDom; PD000252; T_bhtase_apaH; 1.

SMART; SM00054; EFh; 3.

SMART; SM00156; PP2AC; 1.

PROSITE; P80125; SER_THR_PHOSPHATASE;
                                                                                                                                                                                                                                                                                                                                                                        EMBL; CAAI01000476; CAH94488.1; -; InterPro; IPR011992; EF-Hand type. InterPro; IPR002048; EF hand Ca bd. InterPro; IPR004843; M-pesterase. InterPro; IPR006186; T_phtase_apaH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium berghei.
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                    Pfam; PF00036; efhand; 2.
Pfam; PF00149; Metallophos; 1.
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SIMILARITY: Belongs to the PPP
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CATALYTIC ACTIVITY:
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16.8%;
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MEDLINE=22229045; PubMed=11737864; DOI=10.1186/1471-2180-1-31;
A Dobson S., Kar B., Kumar R., Adams B., Barik S.;
T "A novel tetratricopeptide repeat (TPR) containing PP5
T "A novel tetratricopeptide repeat (TPR) containing PP5
T serine/threonine protein phosphatase in the malaria parasite,
T plasmodium falciparum.";
L BMC Microbiol. 1:31-31(2001).
L BMC Microbiol. 1:31-31(2001).
R EMBL; AVO54983; AALI5170.1; -; mRNA.
R GO; GO:0005737; C:cytoplasm; IEA.
R GO; GO:0005737; C:cytoplasm; IEA.
R GO; GO:0005737; F:hydrolase activity; IEA.
R GO; GO:0005737; F:phosphoprotein phosphatase activity; IEA.
R GO; GO:0005731; F:phosphoprotein phosphatase activity; IEA.
R GO; GO:0005731; F:phosphoprotein amino acid dephosphorylation; IEA.
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1.-MAR-2002 (TrEMBLrel. 20, Last sequence up
1.-MAR-2004 (TrEMBLrel. 26, Last annotation
prine/threonine protein phosphatase PP5.
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Best Local Similarity
Matches 151; Conserva
                                                                                                                                                                                                                                                                                                                                                                                           QBIDE7 PLAP7 PRELIMINARY; PRT; (QBIDE7; QBIDE7;   NUCLEOTIDE SEQUENCE.

STRAIN-3D7,

Harris B., Lennard N., Clark L., Line A., Barron A., Corton C.,

Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Dogg

Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.;

Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; ALBA4509; CAD52675.1; -; Genomic_DNA.

HSSP; P36873; 11T6.

GO; GO:0005737; C:cytoplasm; IEA.
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PROSITE; PS50293; TPR REGION;
SEQUENCE 594 AA; 69196 MW;
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Pfam; PF00515; TPR 1; 3.
PIRSF; PIRSF033096; PPPtase
PRINTS; PR00114; STPHPHTASE.
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IPRO01440; TPR.
IPRO06186; T_phtase_apaH.
0149; Metallophos; 1.
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Pred. No. 1.3e-26;
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pfPp5 (EC 3.1.3.16).
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  Name=PpDJ; Synonyms=PPD; ORFNames=CG8402;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygol Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
[1]
                                                                                                                                                                                              UT 30

31 DROME

13 DROME

Q5VH81 DROME PRELIMINARY; PRT; 520 AA.

Q9VH81; Q26244;

01-MAY-2000 (TrEMBLrel. 13, Created)

10-MAY-2000 (TrEMBLrel. 13, Last sequence update)

10-MAY-2005 (TrEMBLrel. 30, Last annotation update)

Protein phosphatase 5 (BC 3.1.3.16) (CG8402-PA, iso)

isoform b) (GH12714p)
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GG; GO:0006731; P:hydrolase activity; IEA.
GO; GO:00064721; P:phosphoprotein phosphatase activity; IEA.
GO; GO:0006470; P:procein amino acid dephosphorylation; IEA.
InterPro; IPR004843; M-pesterase.
InterPro; IPR004843; M-pestase_5.
InterPro; IPR001440; TPR.
InterPro; IPR001440; TPR.
InterPro; IPR00186; T_phtase_apaH.
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PROSITE; PS50293; TPR_REGION;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77; Mismatches 144; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GVMTDLLWSDPNEEKGFKPSK-RGIGFSFGTDITENFL
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                                                                                                               Insecta; Pterygota;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Godayne J.D.,
RA Adams M.D., Celniker S.E., Hilt R.A., Evans C.A., Godayne J.D.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
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RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
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RA Syirskas R., Tector C., Traner R., Venter E., Wang A.H., Wang X.,
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STRAIN=Oregon R; TISSUE=Eye imaginal disc;
STRAIN=Oregon R; TISSUE=Eye imaginal disc;
STRAIN=Oregon R; TISSUE=Eye imaginal disc;
STRAIN=Oregon R; TISSUE=Eye imaginal disc;
MEDLINE=20461855; PubMede1089584; DOI=10.1016/S0167-4781(00)00105-6;
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Biochim. Biophys. Acta 1492:470-476(2000).
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MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J
                                                                                                                                       Patel S., Frise E., Wheeler Ashburner M., Celniker S.E. "The transposable elements
                                                                                                                                                                           NUCLEOTIDE SEQUENCE:
MEDLINB=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., C:
Kaminker J.S., Bergman C.M., Lewis S.E.,
                                                                                                                                                                                                                                                                                                         melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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MEDLINE=22426065; PubMed=12537568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20196006;
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                                                                                           perspective.";
l. 3:RESEARCH0084.1-RESEARCH0084.20(2002)
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  Mungall C.J.,
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                                                                                                                                              of the
                                                                                                                                            Drosophila melanogaster
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    Matthews
                                                                                                                                                                                       Carlson J.W.,
    B.B., Campbell K.S.,
                                                                                                                                                                                                                Svirskas R.,
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Query Match
Best Local S
Matches 136
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005634; F:binding; IEA.
GO; GO:0005488; F:binding; IEA.
GO; GO:0006479; F:hydrolase activity; IEA.
GO; GO:0006470; F:protein amino acid dephosphorylation; IEA.
GO; GO:0006470; F:protein amino acid dephosphorylation; IEA.
GO; GO:0016470; F:protein amino acid dephos
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FlyBase; FBgn0005777; PpD3.
GO; GO:0005737; C:cytoplasm; IE
GO; GO:0005634; C:mucleus; IEA.
GO; GO:0005688; F:binding; IEA.
GO; GO:0016787; F:bydrolase act
GO; GO:0004721; F:phosphoprotein
GO; GO:0006470; P:protein amino
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Ffam; PF00149; Metallophos; 1.
Pfam; PF00515; TPR 1; 3.
PIRSP; PIRSP033096; PPPtase 5; 1.
PRINTS; PR00114; STPHPHTASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O., Schroeder A.J., Schroeder A.J., Schroed
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Celniker S., Carlson J., Wan K., Pfeiffer
Hoskins R., Stapleton M., Pacleb J., Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50005; TPR; 2.
PROSITE; PS50293; TPR_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00156; PP2Ac; 1.
SMART; SM00028; TPR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ensembl; CG8402; Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Berkeley;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AE003684; AAF54438.1; -; Genom
AY058356; AAL13585.1; -; mRNA.
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:|::| ::: | | | ::: | | ::|
    LIDVFRKKRGNRLHPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLL
                                                                                                                                                                                                                                                                                 SAVKADPAYLKGYYRRAAAHMSLGKFKQALCDFEFVAKCR-PNDKDAKLKFTECNKIVKM
                                                                                                                            RAFERAI AVDKPEKT-LSEMYSDMENITIEDDYKGPQLED
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                                                                                                                                                                                                  -HMPQAAGRKNQYQGSAHVSVLDD-KDDLVEEFGDIVNAKIELPIRKNHIDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 577; DB 2;
; Pred. No. 1.2e-26;
83; Mismatches 153
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Svirskas 1
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Mungall C.J.,
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R., Smith E
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Pfam; PF00515; TPR 1; 3.
PIRSF; PIRSF033096; PPPtase_5; 1
PRINTS; PR00114; STPHPHTASE.
SMART; SM00156; PP2AC; 1.
SMART; SM00028; TPR; 3.
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PROSITE; PS50293; TPR REGION;
SEQUENCE 525 AA; 59600 MW;
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Cryptosporidiidae; Cryptosporidium
NCBI TaxID=237895;
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QSCJAB;
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10-MAY-2005 (TEMBLrel. 30,
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STRAIN=TU50
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AAEL01000136; EAL36686.1; -;
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GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0005634; C:nucleus; IEA extivity; IEA.
GO; GO:0016787; F:phosphoprotein phosphatase activity; IGC; GO:0004721; F:phosphoprotein phosphatase activity; IGC; GO:0006470; P:protein amino acid dephosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xu P., Widmer G., Wang Y., Ozaki L.S., Alves J.M., Serrano M.G., Puiu D., Manque P., Akiyoshi D., Mackey A.J., Pearson W.R., Dear Bankier A.T., Peterson D.L., Abrahamsen M.S., Kapur V., Tzipori
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0006470; P:protein amino acid InterPro; IPR004843; M-pesterase. InterPro; IPR011236; PPPtase_5. InterPro; IPR006186; T_phtase_apaH. InterPro; IPR001440; TPR.
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                                                     FIQKWYRRHQARREMOR----RCNWQIFQNLEYASEQDQABLY---
FSKAYYRRGIAYFNLLKYSLARKDFMMVLNLTQNDRDAQSKIQICTKLIKQEKFMDAIST
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                                                                                                       Score 575.5;
Pred. No. 1.5e
57; Mismatches
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Query Match
Best Local Similarity
Matches 120; Conserv
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Pain A., Renauld H., Murphy L., Harris D.A., Quail M.A.,
Hall N., Barrell B.G.;
"The chromosome 2 sequence of Theileria annulata.";
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases
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QAUPS6_1
13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
53-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Serine/threonine protein phosphatase, putative (EC 3.1.3.16).
ORFNames=TA15975;
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                                                                                                                                                                                                         DIHGOFYDLLNIFSINGEPTDENSYLFNGDFYDRGSFSFECVFTLFLAKVLFPSSFHIVR
                                                                                                                                                                                                                                                                                                                 NHLDKSYLPHNTLEYLKVPGNTIHKKYVCMIILEVIKIIREYESVVDLNIYPCDELTVCG
                                                                                                                                                                                                                                                                                                                                                                  NHID---LLIDV--FRKKRGNRLHPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCG
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  ENVTIEDLKKIDRFK--
                                                                                                       GNHETEALNKCYGFKGEILNKY---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                516 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 574.5;
Pred. No. 1.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C670662EEFC4FA55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                    -DEKVYNLFCESFRYLPLGYLINKKVLVIHGGLFGT
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BPSDS---GLMTDMLWSDPKPSNGLSPSK-RGV
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Best Local S
Matches 151
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Mol. Blochem. Parasitol. 120:257-268(2002).

EMBL, AR404815, AR495648.1; -; Genomic_DNA.

HSSP; P36873; 1IT6.
GO; GO:0005747; C:cytoplasm; IEA.
GO; GO:0005747; C:nucleuls; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0016787; F:phosphoprotein phosphatase activity; IEA
GO; GO:0004721; F:phosphoprotein phosphatase activity; IEA
GO; GO:0006470; P:protein amino acid dephosphorylation; IEI
InterPro; IPR014284; M:pesterase.
InterPro; IPR014286; P:protein amino acid dephosphorylation; IEI
InterPro; IPR014286; P:protein amino acid dephosphorylation; IEI
InterPro; IPR014286; P:protein amino acid dephosphorylation; IEI
InterPro; IPR014286; P:protein amino acid dephosphorylation; IEI
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InterPro; IPR014286; P:protein amino acid dephosphorylation; IEI
InterPro; IPR014887; M:pesterase.
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Ffam; PF00515; TPR 1; 3.
PIRSF; PIRSF033096; PPPtcase 5; 1
PRINTS; PR00114; STPHPHTASE.
SMART; SM00156; PP2AC; 1.
SMART; SM00156; PP2AC; 1.
SMART; SM00028; TPR; 3.
PROSITE; PS5005; TPR; 3.
PROSITE; PS50093; TPR REGION; 2.
SEQUENCE 594 AA; 69248 MW; 6
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01-DEC-2001 (TrEMBLrel. 19, Last
01-MAR-2004 (TrEMBLrel. 26, Last
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Q962N7 PLAFA PRELIMINARY;
Q962N7;
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MEDLINE-21896223; PubMed-11897131; DOI-10.1016/S0166-6851(02)00007-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=5833;
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Bukaryota, Alveolata, Apicomplexa, Haemosporida,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=pp5;
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Local Similarity 35.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IRAAIFIQKWYRRHQARREMQRRCNWQIFQNLEYASE--QDQAELYKFFNDLIKHMPQAA 63
FLGELQEKY--DEKMHVLFSDS-FKFLPLAYVLNKNIFICHGGIPSKTDTTLEDIEKIDR
                                              FIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGF--SDSTSLDLIKSIDR
                                                                                                       KINGYPSEKNSYLFNGDFVDRGSFSVEVIIFLYLAKLTFPNNVYLTRGNHETDNMNKIYG
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                                                                                                                                                                                                                                                          ----GNRLHPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLLVVL
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IPR006186; T_phtase_apaH
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Pred. No. 2.3e-
77; Mismatches
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"Oryza sativa BAC OSYMBO0115F21 genomic sequence.";

Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.

BENGL; AC135918; AAV4419-1; -; Genomic DNA.

GO; GO:0005737; C:cytoplasm; IRA.

GO; GO:0005737; C:cytoplasm; IRA.

GO; GO:0004721; F:hydrolase activity; IRA.

GO; GO:0004721; F:hydrolase activity; IRA.

GO; GO:0004721; F:hydrolase activity; IRA.

GO; GO:0004721; F:phosphoportein phosphatase activity; IRA.

GO; GO:0004721; F:phosphoportein phosphatase activity; IRA.

GO; GO:0004721; F:phosphoportein phosphorylation; IRA.

GO; GO:0004721; F:protein amino acid dephosphorylation; IRA.

GO; GO:0004721; F:phosphoportein phosphatase activity; IRA.

GO; GO:0004721; F:protein amino acid dephosphorylation; IRA.

GO; GO:0004721; F:phosphoportein phosphatase activity; IRA.

GO; GO:0004721; F:phosphoportein phosphorylation; IRA.

GO; GO:0004721; F:phosphorylation; IRA.

GO; GO:0004721; F:phosphorylation; IRA.

GO; GO:0004721; F:phosphorylation; 
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Q1-FEB-2005 (TrEMBLrel. 29, Created)

Q1-FEB-2005 (TrEMBLrel. 29, Last sequence update)

Q1-FEB-2005 (TrEMBLrel. 29, Last annotation updat

Putative serine/threenine phosphatase.

Name=OSJNBb0115F21.1;
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PROSITE; PS50293; TPR REGION;
SEQUENCE 483 AA; 54448 MW;
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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69; Mismatches
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                                                                                       A de la Fuente van Bentem S., Vossen J.H., Vermeer J.E.M.,
A de Vroomen M.J., Gadella T.W.J. Jr., Haring M.A., Cornelisse
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AY150041; AAN64317.1; -; mRNA.

REMBL; AY15078; AAN64317.1; -; mRNA.

REMBL; AY182778; AAN64317.1; -; mRNA.

REMBL; AY182778; AAN64317.1; -; Genomic_DNA.

REGO; GO:0005737; C:cytoplasm; IEA.

RGO; GO:0005737; C:cytoplasm; IEA.

RGO; GO:0005737; F:hydrolase activity; IEA.

RGO; GO:0014787; F:hydrolase activity; IEA.

RGO; GO:0014721; F:phospholipase C activity; IEA.

RGO; GO:0007421; F:phosphoprotein phosphatase activity; IEA.

RGO; GO:0007421; F:phosphoprotein phosphatase activity; IEA.

RGO; GO:0007421; F:phosphoprotein phosphatase activity; IEA.

RGO; GO:0007421; F:phosphoprotein phosphatase activity; IEA.

RGO; GO:0007421; F:phosphoprotein phosphatase activity; IEA.

RGO; GO:0007421; F:phosphoprotein phosphatase activity; IEA.

RGO; GO:0007421; F:phosphoprotein phosphatase activity; IEA.

RGO; GO:0007421; F:phosphoprotein phosphorylation; IEA.

RGO; GO:0007421; F:phosphoprotein amino acid dephosphorylation; IEA.

RGO; GO:0007401; F:phosphoprotein amino acid dephosphorylation; IEA.

RR GO; GO:000740; F:protein amino acid dephosphorylation; IEA.

RR InterPro; IPR011236; ppPtase_5.

R InterPro; IPR011236; ppPtase_5.

R InterPro; IPR011236; ppPtase_5; 1.

Pfam; pP00515; TPR 1; 3.

R Pfam; pP00515; TPR 1; 3.

R PINTS; PNR0114; STPHPHTASE;

R PODOM; PD000252; T.phtase_apaH; 1.

RMART; SM00156; PP2AC; 1.

RMART; SM00156; PP2AC; 1.

RAMATI SM00156; PP2AC; 1.
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De La Fuente Van Bentem S., Vossen J.H., Vermeer J.B.,
De La Fuente M.J., Gadella T.W. Jr., Haring M.A., Cornelissen
"The Subcellular Localization of Plant Protein Phosphatase 5
B Determined by Alternative Splicing.";
Plant Physiol. 133:702-712(2003).
PROSITE; PS50007; PIPLC_X_DOMAIN; PROSITE; PS50005; TPR; 3. PROSITE; PS50293; TPR_REGION; 1.
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-2003 (TrEMBLrel. 23, Last sequence update)
-2005 (TrEMBLrel. 29, Last annotation update)
-2005 (TrEMBLrel. 29, Last annotation update)
,serine/threonine phosphatase 55 kDa isoform
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WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
10-MAY-2005 (TrEMBLrel. 30,
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Name=PPP5C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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36.1%; Pred. No. 2.6e-26;
tive 55; Mismatches 124
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R GO; GO:0005737; C:cytoplasm; IRA.

R GO; GO:0005634; C:nucleus; IRA.

R GO; GO:0005684; C:nucleus; IRA.

R GO; GO:0005489; F:bhinding; IRA.

R GO; GO:00064721; F:phosphoprotein phosphatase activity; IRA.

R GO; GO:00064721; F:phosphoprotein phosphatase activity; IRA.

R GO; GO:0006470; P:protein amino acid dephosphorylation; IRA.

R InterPro; IPR004843; M-pesterase.

R InterPro; IPR011236; PPPtase_5.

DR InterPro; IPR011236; PPPtase_5.

R InterPro; IPR011236; TPR-1ike_helical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 143; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00149; Metallophos; 1.
Pfam; PF00515; TPR 1; 3.
PIRSF; PIRSF033096; PPPtase 5; 1.
PRINTS; PR00114; STPHPHTASE.
ProDom; PD000252; T phtase apaH; 1.
SMART; SM00156; PP2AC; 1.
SMART; SM00028; TPR; 3.
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Submitted (
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PROSITE; P850005; TPR, 3.
PROSITE; P850293; TPR_REGION; 1.
Hydrolase; Iron; TPR_repeat.
NON_TER 1 1 1
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Submitted (NOV-2000)
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TISSUE=Muscle;
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     411
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                                        NFLQRHRLSYVIRSHECKPNGHEFMHDNKIITIFSASNYYAIGSNKGAYIRL-NNQLMPH
                                                                                                                                                                                                                              RYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGF--SDSTSLDLIKS
                                                                                                                                                                                                                                                                                                                              ------GSAHV-SVLDDKD----DLVEEFG--DIVNAKIELPIRKNHIDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YIKGYYRRAASNMALGK----FR----AALRD
     AFLEENNLDYIIRSHEVKAEGYEVAHGGRCVTVFSAPNYCDQMGNKASYIHLQGSDLRPQ
                                                                                                                                             IDRGKYVSILRPPLTDGBPLDKTEWQQIFDIMWSDPQATMGCVPNTLRGAGVWPGPDVTD
                                                                                                                                                                                                  IYGFEGEVKAKYT---AQMYELFSEVFEWLPLAQCINGKVLIMHGGLFSEDGVTLDDIRK
                                                                                                                                                                                                                                                                                                  NIFELNGLPSETNPY I FNGDFVDRGSFSVEVILTLFGFKLLYPDHFHLLRGNHETDNMNQ
                                                                                                                                                                                                                                                                                                                                                                                             LMQWYKDQK--KLHRKCAYQILVQVKEVLSKLSTLVETTLKETEKITVCGDTHGQFYDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                        LIDVFRKKRGNRLHPKYVALILRBAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLL
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                                                                                                     -DSGPM-----CDLLWSDPQPQNG-RSISKRGVSCQFGPDVTK
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Pred. No. 2.8e-26;
1; Mismatches 142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----YETVVKVKPHDKDAKMKYQ
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PPP5_HUMAN
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                                                                                                                                                                                                                           PubMed=1557824; DOI-10.1038/nature02399;

AG Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,

AG Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,

AA Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,

AA Caenepeel S., Carrano A.V., Caoile C., Chan Y.M., Christensen M.,

Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Detter J.C.,

Bscobar J., Plowers D., Fotopulos D., Garcia C., Georgescu A.M.,

Caenepeel S., Carrano A.V., Caoile C., Chan Y.M., Christensen M.,

AR Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Detter J.C.,

AB Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,

AG Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,

AR Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,

AR Kobayashi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,

AM Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J.,

AR Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J.,

AR Noglie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,

AR Noglie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,

AR Noglie A.P., Predki P., Quan G., Ramirez L., She X., Smith D.,

Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A.,

Vo N., Wagner M., Meeler J., Wu K., Xie G., Yang J., Dubchak I.,

Purey T.S., DeJong P., Dickson M., Gordon D., Eichler E.E.,

"The DNA sequence and biology of human chromosome 19.",

Nature 428:529-535(2004).
MEDLINE-22386257; PubMed-12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E srownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPP5 HUMAN STANDARD; PRT; 4
F53041; Q16722;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
13-SEP-2005 (Rel. 48, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Fetal brain;
MEDLINE-96115607; PubMed-8666404;
YONG W.H., Ueki K., Chou D., Reeves S.A., von Deimling A.,
Gusella J.F., Mohrenweiser H.W., Buckler A.J., Louis D.N.;
"Cloning of a highly conserved human protein serine-threonine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A novel human protein serine/threonine phosphatase, which possesses four tetratricopeptide repeat motifs and localizes to the nucleus."; EMBO J. 13:4278-4290(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Serine/threonine protein phosphatase phosphatase T) (PP-T) (PPT).
Name=PPP5C; Synonyms=PPP5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphatase gene
19q13.3.";
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NUCLEOTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE OF 7-499.
MEDLINE=95009929; PubMed=7925273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29:533-536(1995).
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                                                                                                                                                                                            SEQUENCE [LARGE SCALE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOI=10.1038/nature02399;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.E., Brown
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                                                                                                                                                                                          MRNA].
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= 5 (EC 3.1
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                            ng L.,
Scheetz T.E.,
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PDB; 1A17; X-ray; @=16-181.

PDB; 1S95; X-ray; A/B=169-499.

PDB; 1WAO; X-ray; 1/2/3/4=23-499.

SMR; P53041; 23-499.

Ensembl; ENSG00000011485; Homo Bapiens.

HGNC; HGNC:9322; PPP5C.

HGNC; HGNC:9322; PPP: H-InvDB; HIX0015250;

GO:0005634; C:nucleus; GO:0004722; F:protein;

TAS

serine/threonine phosphatase activity;

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EMBL; X89416; CAA61595.1; -; mRNA.
EMBL; U25174; AAB60384.1; -; mRNA.
EMBL; U25174; AAB60384.1; -; mRNA.
EMBL; BC007193; AAD22669.1; -; mRNA.
EMBL; BC001970; AAH01970.1; -; mRNA.
EMBL; X92121; CAA63089.1; -; mRNA.
PIR; X52570; S52570;
PDB; 1A17; X-ray; @=16-181.
PDB; 1A17; X-ray; 0=16-181.
PDB; 1A30; X-ray; A/B=169-499.
PDB; 1A00; X-ray; A/B=169-499.
SMR; P53041; 23-499.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bossk S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Balkesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B., Schmerch A., Schein J.B., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                This Swiss-Prot entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are r

    -I- FUNCTION: May play a role in the regulation of RNA bioger
and/or mitosis. In vitro, dephosphorylates serine residue
skeletal muscle phosphorylase and histome H1.
    -I- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98151343; PubMed=9482716; DOI=10.1093/emboj/17.5.1192; Das A.K., Cohen P.W., Barford D.; "The structure of the tetratricopeptide repeats of protein phoses: implications for TPR-mediated protein-protein interactions." EMBO J. 17:1192-1199(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Fetal brain;
MEDLINE=96144708; PubMed=8561788; DOI=10.1006/bbrc.1996.0092;
Nn X.. Lagercrantz J., Zickert P., Bajalica-Lagercrantz S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          two tetratricopeptide repeat-containing promoting complex.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98070360; PubMed=9405
Ollendorff V., Donoghue D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              serine/threonine phosphatase
Biochem. Biophys. Res. Commur
                                                                                                                                                                                                                                                                                  removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Chromosomal localization and
                                                                                                                                                                                                                                                                                                                                                                              the cytoplasm.
TISSUE SPECIFICITY: Ubiquitous.
SIMILARITY: Belongs to the PPP phosphatase
SIMILARITY: Contains 3 TPR repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COPACTOR: Binds 1 iron ion per subunit (By sim COPACTOR: Binds 1 manganese ion per subunit (E SUBUNIT: Interacts with CDC16 and CDC27. SUBCELLULAR LOCATION: Nuclear; predominantly,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Natl. Acad.
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0360; PubMed=9405394;
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218:514-517(1996)
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InterPro; IPRO1440; TPR.
InterPro; IPRO11490; TPR-like helical
Pfam; PP00149; Metallophos; 1.
Pfam; PP001515; TPR 1; 3.
PIRSP; PIRSP031906; PPPCase 5; 1.
PRINTS; PRO0114; STPHPHTASE.
PRODOM; PD000252; T phtase apah; 1.
SMART; SM00156; PPAC; 1.
SMART; SM00028; TPR; 3.
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GO; GO:0007067; P:mitosis; TAS.
GO; GO:0043123; P:positive regulati GO; GO:006470; P:protein amino aci GO; GO:0006350; P:transcription; TA InterPro; IPR004843; M-pesterase. InterPro; IPR004843; M-pesterase. InterPro; IPR006186; T_phtase_apaH.
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PROSITE; PS50005; TPR; 3.
PROSITE; PS50293; TPR_REGION; 1.
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                                   RYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGF--SDSTSLDLIKS
                                                                                              LIDVFRKKRGNRLHPKYVALILRBAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLL
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TPR 1.
TPR 2.
TPR 3.
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; Pred. No. 2.9e-26;
71; Mismatches 142
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Iron and manganese (By similarity).
Manganese (By similarity).
Manganese (By similarity).
Manganese (By similarity).
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ARTYMANA K., SUMMAN A., SUMMAN 
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Best Loc
Matches
            phosphate.

-1- SIMILARITY: Belongs to the PPP phosphatase family.

EMBL; BT007275; AAP35939.1; -; mRNA.

SMR; Q53XV2; 23-499.

Ensembl; ENSG0000011485; Homo sapiens.

GO; GO:0005737; C:cytoplasm; IEA.

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0004721; F:phosphoprotein phosphatase activity; IEA.

GO; GO:0004707; P:protein amino acid dephosphorylation; IER

InterPro; IPR004843; M-pesterase.

InterPro; IPR00186; TpR.

InterPro; IPR001890; TPR.-like_helical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               i3-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Protein phosphatase 5, catalytic subunit.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                       Submitted (MAY-2003) to -1- CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kalnine N., Chen X., Rolfs A., Halleck A., Hines Koundinya M., Raphael J., Moreira D., Kelley T., Phelan M., Farmer A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q53XV2 HUMAN PRBLIMINARY;
Q53XV2;
                                                                                                                                                                                                                                                                                                                                                                                                            vector.
                                                                                                                                                                                                                                                                                                                                                                                                                           Phelan M., Farmer A.; "Cloning of human full-length CDSs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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33.7%;
          T_phtase_apaH.
TPR.
TPR-like_helical
                                                                                                                                                                                                                                                                                                                                                       the EMBL/GenBank/DDBJ databases.
A phosphoprotein + H(2)O = a pro
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Pred. No. 2.9e-26;
1; Mismatches 142
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RESULT 40
Q64538 RAT
ID 464538;
AC Q64538;
DT 01-NOV-1996 (TrEMBLrel. 01, C)
DT 01-FEB-1997 (TrEMBLrel. 26, Li
DT 01-FEB-1997 (TrEMBLrel. 26, Li
DT 01-FEB-1997 (TrEMBLrel. 26, Li
DT 01-MAR-2004 (TrEMBLrel. 26, Li
DT 01-MAR-2004 (TrEMBLrel. 26, Li
DT 01-MAR-2004 (TrEMBLrel. 26, Li
DT 01-MAR-2004 (TrEMBLrel. 26, Li
DT 01-FEB-1997 (TREMBLREL)
CO Rattus norvegicus (Rat)
CO Eukaryotta; Metazoa; Chordata;
CO Muridae; Murinae; Rattus.
CO Muridae; Murinae; Rattus.
CO MURIDENTIDE SEQUENCE.
RN (1)
RP NUCLEOTIDE SEQUENCE.
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAINS-Sprague-Dawley; TISSUE
RX MCDLINE-95062208; PubMed-7972
RA MEDLINE-95062208; PubMed-7972
RA MEDLINE-95062208; PubMed-7972
RA FI "Targeting of a distinctive p
RT winase-like domain of the atr
Proc. Natl. Acad. Sci. U.S.A.
CC -i- CATALYTIC ACTIVITY: A pho
CC -i- SIMILARITY: Belongs to th
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Best Local Similarity
Matches 143; Conserv
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Pfam; PF00515; TPR 1; 3.
PRINTS; PR00114; STPHPITASB.
ProDom; PR001252; T_phtase_apaH; 1.
SMART; SM00156; PP2Ac; 1.
SMART; SM000256; TPR; 3.
PROSITE; PS00125; SER THR_PHOSPHATASE; UN PROSITE; PS00125; SER THR_PTOSPHATASE; UN PROSITE; PS50293; TPR_REGION; 1.
Hydrolase; Iron; Repeat; TPR repeat
SEQUENCE 499 AA; 56879 MW; DB3B2090DE
                                                       "Targeting of a distinctive protein-serine phosphatase to the kinase-like domain of the atrial natriuretic peptide receptor. Proc. Natl. Acad. Sci. U.S.A. 91:11075-11079(1994).
-i- CATALYTIC ACTIVITY: A phosphoprotein + H(2)0 = a protein +
                                                                                                                                                                               STRAIN=Sprague-Dawley; TISSUE=Lung; MEDLINE=95062208; PubMed=7972012;
                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurogna Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LMQWYKDQK--KLHRKCAYQILVQVKEVLSKLSTLVETTLKETEKITVCGDTHGQFYDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIDVFRKKRGNRLHPKYVALILRBAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ECNKIVKOKAFERAIAGDEHKRSVVDSLDIESMTIEDEYSGPKLEDGKVTISFMKE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -dab-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSGPM-----CDLLWSDPQPQNG-RSISKRGVSCQFGPDVTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -GSAHV-SVLDDKD----DLVEBFG--DIVNAKIELPIRKNHIDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71;
            the PPP phosphatase family
                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update), Last annotation updat (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 570; DB
Pred. No. 2.9e
71; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat.
; DB3B2090D8658BB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  570; DB 2;
No. 2.9e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142;
                                                                                                                                                                                                                                                                                                                                                                                                                      update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                            Sciurognathi;
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368 345 285

107 193 167 251 227

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RHSSP; P53041; 1A17.

RSMR; Q64538; 3-479.

RGO; G0:0005737; C:cyytoplasm; IEA.

RGO; G0:0005634; C:nucleus; IEA.

RGO; G0:0005488; F:binding; IEA.

RGO; G0:0006470; P:phosphoprotein phosphatase activity; IEA.

RGO; G0:0006470; P:protein amino acid dephosphorylation; IEA.

RGO; G0:0006470; P:protein amino acid dephosphorylation; IEA.

RINTERPO; IPRO01440; TPR.

RINTERPO; IPRO01440; TPR.

RINTERPO; IPRO0140; TPR.

RINTERPO; IPRO11990; TRP-1ike helical.

RPfam; PF00149; Metallophos; 1.

RPfam; PF00515; TRP. 1; 3.

RPINTS; PR00114; STPHPHTASE.

PRODOm; PD000252; T phtase_apaH; 1.

SMART; SM00015; TPR, 3.

RPROSITE; PS00125; SER THR PHOSPHATASE; UNKNOWN_1.

RPROSITE; PS00125; SER THR PHOSPHATASE; UNKNOWN_1.

RPROSITE; PS000125; SER THR PROSPHATASE; UNKNOWN_1.

RPROSITE; PS00125; SER THR PHOSPHATASE; UNKNOWN_1.

RPROSITE; PS02023; TPR_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 143; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                        393 AFLEENQLDYIIRSHEVKAEGYEVAHGGRCVTVFSAPNYCDQMGNKASYIHLQGSDLRPQ 452
                                                                                            346 NFLQRHRLSYVIRSHECKPNGHEFWHDNKIITIFSASNYYAIGSNKGAYIRL-NNQLMPH 404
                                                                                                                                            349 IERNR-----QPP--DSGPM------CDLLWSDPQPQNGRSVSK-RGVSCQFGPDVTK 392
                                                                                                                                                                           286 IDRGKYVSILRPPLTDGEPLDKTEWQQIFDIMWSDPQATMGCVPNTLRGAGVWFGPDVTD 345
                                                                                                                                                                                                                     292 IYGFEGEVKAKYI---AQMYELFSEVFEMLPLAQCINGKYLIMHGGLFSEDGVTLDDIRK 348
                                                                                                                                                                                                                                                        228 RYGFIREVESKYPRNHKRILAFIDEVYRWLPLGSVLNSRVLIVHGGF--SDSTSLDLIKS 285
                                                                                                                                                                                                                                                                                                                                                                     174 LMQMYKDQK--KLHRKCAYQILVQVKEVLCKLSTLVETTLKETEKITVCGDTHGQFYDLL
                                                                                                                                                                                                                                                                                                                                                                                                      108 LIDVFRKKRGNRLHPKYVALILREAAKSLKQLPNISPVSTAVSQQVTVCGDLHGKLDDLL 167
453
                                405 FVQY 408
                                                                                                                                                                                                                                                                                                                                                                                                                                              118 ECSKIVKQKAFERAIAGDEHRRSVVDSLDIESMTIEDEYSGPKLEDGKVTITFMKD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 YİKGYYRRAASIMALGK-----FR----AALRD-----YETVVKVKPIDKDAKMKYQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 FIQKWYRRHQARREMQRRCNWQIFQNLEYASEQDQAELYKFFNDLIKHMPQAAGRKNQYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 -----GSAH-VSVLDDKD----DLVEEFG--DIVNAKIELPIRKNHIDL 107
FHQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  479 AA; 54718 MW; 173CAD1EEF526450 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.5%; Score 569; DB 2; Length 479; ilarity 33.7%; Pred. No. 3.2e-26; Conservative 73; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              173
                                                                                                                                                                                                                                                                                                                                                                     231
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Search completed: January 20, 2006, 19:51:54 Job time : 170 secs